

RAW SEQUENCE LISTING PATENT APPLICATION US/08/083,590

DATE: 12/16/93 TIME: 13:07:45

1		SEQUENCE LISTING	P
3	(1) G	eneral Information:	
4 5 6	(i)	APPLICANT: Artavanis-Tsakonas, S. et al.	
7 8 9 10 11	(ii)	TITLE OF INVENTION: Therapeutic And Diagnostic Methods And Compositions Based On Notch Proteins And Nucleic Acids	3
12 13	(iii)	NUMBER OF SEQUENCES: 21	
14 15 16 17 18 19 20	(iv)	CORRESPONDENCE ADDRESS: (A) ADDRESSEE: Pennie & Edmonds (B) STREET: 1155 Avenue of the Americas (C) CITY: New York (D) STATE: New York (E) COUNTRY: U.S.A. (F) ZIP: 10036	
22 23 24 25 26 27	(v)	COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: PatentIn Release #1.0, Version #1.25	
28 29 30 31 32	(vi)	CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: 08/083,590 (B) FILING DATE: 25-JUN-1993 (C) CLASSIFICATION:	
32 33 34 35 36 37 38 39		ATTORNEY/AGENT INFORMATION: (A) NAME: Misrock, S. Leslie (B) REGISTRATION NUMBER: 18,872 (C) REFERENCE/DOCKET NUMBER: 7326-015 TELECOMMUNICATION INFORMATION: (A) TELEPHONE: 212 790-9090	
40 41 42 43 44	(2) INFO	(B) TELEFAX: 212 8698864/9741 (C) TELEX: 66141 PENNIE RMATION FOR SEQ ID NO:1:	
44 45 46 47 48 49 50		SEQUENCE CHARACTERISTICS: (A) LENGTH: 2892 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: unknown	

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52 53		(ii)) MO:	LECU	LE T	YPE:	cDN	A									
54 55 56 57 58		(ix	()	ATURI A) N B) L	AME/I			264	10								
59 60		(xi)) SE	QUEN	CE DI	ESCR	IPTI	ON:	SEQ :	ID N	0:1:						
61 62 63	GAA:	rtcg	GAG (GAAT'	TATT	CA A	AACA'	AAAT	C AC	ATA	AACA	ATT:	rgag:	rag :	rtgco	CGCACA	60
64 65	CAC	ACAC	ACA (CACA	GCCC	GT G	GATT	ATTA	C AC'	TAAA	AGCG	ACA	CTCA	ATC (CAAA	AAATCA	120
66 67 68 69	GCA	ACAA	AAA (CATC	ATAA	AA C				ATT Ile							171
70 71 72 73				TTC Phe													219
74 75 76 77				CTG Leu 30													267
78 79 80 81				TGC Cys													315
82 83 84 85				AAG Lys													363
86 87 88 89				ACC Thr													411
90 91 92 93				GAG Glu													459
94 95 96 97				TTC Phe 110													507
98 99 100 101				TTC Phe													555
102	AGC	GGC	AAT	GCG	CGA	ACC	AAC	AAG	CTC	CTC	ATC	CAG	CGA	CTC	TTG	GTG	603

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103 104 105	Ser	Gly 140	Asn	Ala	Arg	Thr	Asn 145	Lys	Leu	Leu	Ile	Gln 150	Arg	Leu	Leu	Val		
106 107 108 109					GAG Glu												651	
110 111 112 113					TCG Ser 175												699	
114 115 116 117					TCC Ser												747	
118 119 120 121					TCG Ser												795	
122 123 124 125					GGC Gly												843	
126 127 128 129					CAT His												891	
130 131 132 133					GCC Ala 255												939	
134 135 136 137					TGC Cys												987	
138 139 140 141					TAC Tyr												1035	
142 143 144 145					AAT Asn												1083	
146 147 148 149					TGC Cys												1131	
150 151 152 153					TGC Cys 335												1179	

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INPUT SET: S7068.raw

154 155 156		ATC Ile							1227
157 158 159 160 161		GGC Gly 365							1275
162 163 164 165		AAA Lys							1323
166 167 168 169		AGC Ser							1371
170 171 172 173		CCC Pro							1419
174 175 176 177		AAC Asn							1467
178 179 180 181		TTT Phe 445							1515
182 183 184 185		CAG Gln							1563
186 187 188 189		TGC Cys							1611
190 191 192 193	_	GAC Asp							1659
194 195 196 197		CTC Leu							1707
198 199 200 201		GAT Asp 525							1755
201 202 203 204		GGC Gly							1803

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205																	
206	TGT	GCC	AAT	GGT	TTC	AGG	GGC	AAG	CAG	TGC	GAT	GAG	GAG	TCC	TAC	GAT	1851
207						Arg											
208	555					560	_	_		_	565				-	570	
209																	
210	TCG	GTG	ACC	TTC	GAT	GCC	CAC	CAA	TAT	GGA	GCG	ACC	ACA	CAA	GCG	AGA	1899
211		_				Ala											
212					575					580					585	J	
213																	
214	GCC	GAT	GGT	TTG	ACC	AAT	GCC	CAG	GTA	GTC	CTA	ATT	GCT	GTT	TTC	TCC	1947
215	Ala	Asp	Gly	Leu	Thr	Asn	Ala	Gln	Val	Val	Leu	Ile	Ala	Val	Phe	Ser	
216				590					595					600			
217																	
218	GTT	GCG	ATG	CCT	TTG	GTG	GCG	GTT	ATT	GCG	GCG	TGC	GTG	GTC	TTC	TGC	1995
219	Val	Ala	Met	Pro	Leu	Val	Ala	Val	Ile	Ala	Ala	Cys	Val	Val	Phe	Cys	
220			605					610					615			_	
221																	
222	ATG	AAG	CGC	AAG	CGT	AAG	CGT	GCT	CAG	GAA	AAG	GAC	GAC	GCG	GAG	GCC	2043
223	Met	Lys	Arg	Lys	Arg	Lys	Arg	Ala	Gln	Glu	Lys	Asp	Asp	Ala	Glu	Ala	
224		620					625					630					
225																	
226	AGG	AAG	CAG	AAC	GAA	CAG	AAT	GCG	GTG	GCC	ACA	ATG	CAT	CAC	AAT	GGC	2091
227	Arg	Lys	Gln	Asn	Glu	Gln	Asn	Ala	Val	Ala	Thr	Met	His	His	Asn	Gly	
228	635					640					645					650	
229																	
230	AGT	GGG	GTG	GGT	GTA	GCT	TTG	GCT	TCA	GCC	TCT	CTG	GGC	GGC	AAA	ACT	2139
231	Ser	Gly	Val	Gly	Val	Ala	Leu	Ala	Ser	Ala	Ser	Leu	Gly	Gly	Lys	Thr	
232					655					660					665		
233																	
234	GGC	AGC	AAC	AGC	GGT	CTC	ACC	TTC	GAT	GGC	GGC	AAC	CCG	AAT	ATC	ATC	2187
235	Gly	Ser	Asn	Ser	Gly	Leu	Thr	Phe	Asp	Gly	Gly	Asn	Pro	Asn	Ile	Ile	
236				670					675					680			
237																	
238						AAG											2235
239	Lys	Asn		Trp	Asp	Lys	Ser		Asn	Asn	Ile	Cys	Ala	Ser	Ala	Ala	
240			685					690					695				
241																	
242						GCA											2283
243	Ala		Ala	Ala	Ala	Ala		Ala	Ala	Asp	Glu	_	Leu	Met	Tyr	Gly	
244		700					705					710					
245																	
246						GTG											2331
247	_	Tyr	Val	Ala	Ser	Val	Ala	Asp	Asn	Asn		Ala	Asn	Ser	Asp		
248	715					720					725					730	
249		~-~	~~-		a	a		~~~		me	a		a. -	-			
250						CAA											2379
251	cys	vaı	АТА	Pro		Gln	Arg	Ala	гàг		GIN	гàг	GIN	ьeu		Tnr	
252					735					740					745		
253 254	CI N TH	aaa	700	CmC	א שיכי	C7 C	aaa	dam	maa	aaa	CC2	aaa	700	ጥር ላ	aaa	אאכ	2427
25 4 255						CAC His											2427
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262		COO TOO TIME COO 2522
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266		ATG GCT GCA GCT 2571
267		
268		810
269		010
270	TCG GCA GCG GGC AGC GGA GCG GGG ACG GCG CAA CAG	CAG CGA TCC GTG 2619
271		
272	1 1	825
273		
274	GTC TGC GGC ACT CCG CAT ATG TAACTCCAAA AATCCGGA	AG GGCTCCTGGT 2670
275	Val Cys Gly Thr Pro His Met	
276		
277		
278	AAATCCGGAG AAATCCGCAT GGAGGAGCTG ACAGCACATA CAC	AAAGAAA AGACTGGGTT 2730
279		
280	GGGTTCAAAA TGTGAGAGAG ACGCCAAAAT GTTGTTGTTG ATT	GAAGCAG TTTAGTCGTC 2790
281		
282	ACGAAAAATG AAAAATCTGT AACAGGCATA ACTCGTAAAC TCC	CTAAAAA ATTTGTATAG 2850
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293		
294	(ii) MOLECULE TYPE: protein	
295	() GEOMENGE DEGGETDETON, GEO. TD NO. 3	
296 297		
		Gree The Mhrs II-1
298	Met His Trp Ile Lys Cys Leu Leu Thr Ala Phe Ile	_
299		15
300 301		Ara Iou Iva Tre
301		
302		30
303		Cve Cve Ser Clu
304		45
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307 308 309	Glu	Ser 50	Asp	Gly	Ala	Thr	Gly 55	Lys	Суѕ	Leu	Gly	Ser 60	Cys	Lys	Thr	Arg
310 311 312	Phe 65	Arg	Val	Cys	Leu	Lys 70	His	Tyr	Gln	Ala	Thr 75	Ile	Asp	Thr	Thr	Ser 80
313 314 315	Gln	Cys	Thr	Tyr	Gly 85	Asp	Val	Ile	Thr	Pro 90	Ile	Leu	Gly	Glu	Asn 95	Ser
316 317 318	Val	Asn	Leu	Thr 100	Asp	Ala	Gln	Arg	Phe 105	Gln	Asn	Lys	Gly	Phe 110	Thr	Asn
319 320 321	Pro	Ile	Gln 115	Phe	Pro	Phe	Ser	Phe 120	Ser	Trp	Pro	Gly	Thr 125	Phe	Ser	Leu
322 323 324	Ile	Val 130	Glu	Ala	Trp	His	Asp 135	Thr	Asn	Asn	Ser	Gly 140	Asn	Ala	Arg	Thr
325 326 327	Asn 145	Lys	Leu	Leu	Ile	Gln 150	Arg	Leu	Leu	Val	Gln 155	Gln	Val	Leu	Glu	Val 160
328 329 330	Ser	Ser	Glu	Trp	Lys 165	Thr	Asn	Lys	Ser	Glu 170	Ser	Gln	Tyr	Thr	Ser 175	Leu
331 332 333	Glu	Tyr	Asp	Phe 180	Arg	Val	Thr	Cys	Asp 185	Leu	Asn	Tyr	Tyr	Gly 190	Ser	Gly
334 335 336	Cys	Ala	Lys 195	Phe	Сув	Arg	Pro	Arg 200	Asp	Asp	Ser	Phe	Gly 205	His	Ser	Thr
337 338 339	Cys	Ser 210	Glu	Thr	Gly	Glu	Ile 215	Ile	Cys	Leu	Thr	Gly 220	Trp	Gln	Gly	Asp
340 341 342	Tyr 225	Cys	His	Ile	Pro	Lys 230	Cys	Ala	Lys	Gly	Cys 235	Glu	His	Gly	His	Cys 240
343 344 345	Asp	Lys	Pro	Asn	Gln 245	Cys	Val	Cys	Gln	Leu 250	Gly	Trp	Lys	Gly	Ala 255	Leu
346 347 348	Cys	Asn	Glu	Cys 260		Leu	Glu		Asn 265		Ile	His	Gly	Thr 270		Asn
349 350 351	Lys	Pro	Trp 275	Thr	Cys	Ile	Cys	Asn 280	Glu	Gly	Trp	Gly	Gly 285	Leu	Tyr	Cys
352 353 354	Asn	Gln 290	Asp	Leu	Asn	Tyr	Cys 295	Thr	Asn	His	Arg	Pro 300	Cys	Lys	Asn	Gly
355 356 357	Gly 305	Thr	Cys	Phe	Asn	Thr 310	Gly	Glu	Gly	Leu	Tyr 315	Thr	Cys	Lys	Cys	Ala 320

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358 359 360	Pro	Gly	Tyr	Ser	Gly 325	Asp	Asp	Cys	Glu	Asn 330	Glu	Ile	Tyr	Ser	Cys 335	Asp
361 362 363	Ala	Asp	Val	Asn 340	Pro	Cys	Gln	Asn	Gly 345	Gly	Thr	Cys	Ile	Asp 350	Glu	Pro
364 365 366	His	Thr	Lys 355	Thr	Gly	Tyr	Lys	Cys 360	His	Cys	Ala	Asn	Gly 365	Trp	Ser	Gly
367 368 369	Lys	Met 370	Cys	Glu	Glu	Lys	Val 375	Leu	Thr	Cys	Ser	Asp 380	Lys	Pro	Cys	His
370 371 372	Gln 385	Gly	Ile	Cys	Arg	Asn 390	Val	Arg	Pro	Gly	Leu 395	Gly	Ser	Lys	Gly	Gln 400
373 374 375	Gly	Tyr	Gln	Cys	Glu 405	Cys	Pro	Ile	Gly	Tyr 410	Ser	Gly	Pro	Asn	Cys 415	Asp
376 377 378	Leu	Gln	Leu	Asp 420	Asn	Cys	Ser	Pro	Asn 425	Pro	Cys	Ile	Asn	Gly 430	Gly	Ser
379 380 381	Cys	Gln	Pro 435	Ser	Gly	Lys	Cys	Ile 440	Cys	Pro	Ala	Gly	Phe 445	Ser	Gly	Thr
382 383 384	Arg	Cys 450	Glu	Thr	Asn	Ile	Asp 455	Asp	Cys	Leu	Gly	His 460	Gln	Cys	Glu	Asn
385 386 387	Gly 465	Gly	Thr	Cys	Ile	Asp 470	Met	Val	Asn	Gln	Tyr 475	Arg	Cys	Gln	Cys	Val 480
388 389 390	Pro	Gly	Phe	His	Gly 485	Thr	His	Cys	Ser	Ser 490	Lys	Val	Asp	Leu	Cys 495	Leu
391 392 393	Ile	Arg	Pro	Cys 500	Ala	Asn	Gly	Gly	Thr 505	Cys	Leu	Asn	Leu	Asn 510	Asn	Asp
394 395 396	Tyr	Gln	Cys 515	Thr	Cys	Arg	Ala	Gly 520	Phe	Thr	Gly	Lys	Asp 525	Cys	Ser	Val
397 398 399	Asp	Ile 530		Glu	Cys		Ser 535	_	Pro	Cys		Asn 540	-	Gly	Thr	Cys
400 401 402	Met 545	Asn	Arg	Val	Asn	Ser 550	Phe	Glu	Cys	Val	Cys 555	Ala	Asn	Gly	Phe	Arg 560
403 404 405	Gly	Lys	Gln	Cys	Asp 565	Glu	Glu	Ser	Tyr	Asp 570	Ser	Val	Thr	Phe	Asp 575	Ala
406 407 408	His	Gln	Tyr	Gly 580	Ala	Thr	Thr	Gln	Ala 585	Arg	Ala	Asp	Gly	Leu 590	Thr	Asn

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409 410 411	Ala	Gln	Val 595	Val	Leu	Ile	Ala	Val 600	Phe	Ser	Val	Ala	Met 605	Pro	Leu	Val
412 413 414	Ala	Val 610	Ile	Ala	Ala	Cys	Val 615	Val	Phe	Cys	Met	Lys 620	Arg	Lys	Arg	Lys
415 416 417	Arg 625	Ala	Gln	Glu	Lys	Asp 630	Asp	Ala	Glu	Ala	Arg 635	Lys	Gln	Asn	Glu	Gln 640
418 419 420	Asn	Ala	Val	Ala	Thr 645	Met	His	His	Asn	Gly 650	Ser	Gly	Val	Gly	Val 655	Ala
421 422 423	Leu	Ala	Ser	Ala 660	Ser	Leu	Gly	Gly	Lys 665	Thr	Gly	Ser	Asn	Ser 670	Gly	Leu
424 425 426	Thr	Phe	Asp 675	Gly	Gly	Asn	Pro	Asn 680	Ile	Ile	Lys	Asn	Thr 685	Trp	Asp	Lys
427 428 429		Val 690				_	695					700				
430 431 432	Ala 705	Ala	Ala	Asp	Glu	Cys 710	Leu	Met	Tyr	Gly	Gly 7 1 5	Tyr	Val	Ala	Ser	Val 720
433 434 435	Ala	Asp	Asn	Asn	Asn 725	Ala	Asn	Ser	Asp	Phe 730	Сув	Val	Ala	Pro	Leu 735	Gln
436 437 438	Arg	Ala	Lys	Ser 740	Gln	Lys	Gln	Leu	Asn 745	Thr	Asp	Pro	Thr	Leu 750	Met	His
439 440 441	Arg	Gly	Ser 755	Pro	Ala	Gly	Ser	Ser 760	Ala	Lys	Gly	Ala	Ser 765	Gly	Gly	Gly
442 443 444	Pro	Gly 770	Ala	Ala	Glu	Gly	Lys 775	Arg	Ile	Ser	Val	Leu 780	Gly	Glu	Gly	Ser
445 446 447	Tyr 785	Cys	Ser	Gln	Arg	Trp 790	Pro	Ser	Leu	Ala	Ala 795	Ala	Gly	Val	Ala	Gly 800
448 449 450	Ala	Cys	Ser	Ser	Gln 805		Met	Ala	Ala		Ser			_	Ser 815	-
451 452 453	Ala	Gly	Thr	Ala 820	Gln	Gln	Gln	Arg	Ser 825	Val	Val	Cys	Gly	Thr 830	Pro	His
454 455 456	Met															
457 458	(2)	INFO	ORMAT	rion	FOR	SEQ	ID 1	10:3	:							
459		(i)	SEÇ	QUENC	CE CE	IARAC	CTER	STIC	CS:							

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DATE: 12/16/93 TIME: 13:08:42

460 461 462 463 464	(A) LENGTH: 1320 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: unknown	
465 466	(ii) MOLECULE TYPE: cDNA	
467 468 469 470 471 472	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 4421320	
473 474 475	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
476	CCGAGTCGAG CGCCGTGCTT CGAGCGGTGA TGAGCCCCTT TTCTGTCAAC GCTAAAGATC	60
477 478 479	TACAAAACAT CAGCGCCTAT CAAGTGGAAG TGTCAAGTGT GAACAAAACA AAAACGAGAG	120
480	AAGCACATAC TAAGGTCCAT ATAAATAATA AATAATAATT GTGTGTGATA ACAACATTAT	180
481 482	CCAAACAAAA CCAAACAAAA CGAAGGCAAA GTGGAGAAAA TGATACAGCA TCCAGAGTAC	240
483 484	GGCCGTTATT CAGCTATCCA GAGCAAGTGT AGTGTGGCAA AATAGAAACA AACAAAGGCA	300
485 486	CCAAAATCTG CATACATGGG CTAATTAAGG CTGCCCAGCG AATTTACATT TGTGTGGTGC	360
487 488	CAATCCAGAG TGAATCCGAA ACAAACTCCA TCTAGATCGC CAACCAGCAT CACGCTCGCA	420
489 490 491 492 493	AACGCCCCCA GAATGTACAA A ATG TTT AGG AAA CAT TTT CGG CGA AAA CCA Met Phe Arg Lys His Phe Arg Arg Lys Pro 1 5 10	471
494 495 496 497	GCT ACG TCG TCG TCG GAG TCA ACA ATA GAA TCA GCA GAC AGC CTG Ala Thr Ser Ser Leu Glu Ser Thr Ile Glu Ser Ala Asp Ser Leu 15 20 25	519
498 499 500 501	GGA ATG TCC AAG AAG ACG GCG ACA AAA AGG CAG CGT CCG AGG CAT CGG Gly Met Ser Lys Lys Thr Ala Thr Lys Arg Gln Arg Pro Arg His Arg 30 35 40	567
502 503 504 505	GTA CCC AAA ATC GCG ACC CTG CCA TCG ACG ATC CGC GAT TGT CGA TCA Val Pro Lys Ile Ala Thr Leu Pro Ser Thr Ile Arg Asp Cys Arg Ser 45 50 55	615
506 507 508	TTA AAG TCT GCC TGC AAC TTA ATT GCT TTA ATT TTA ATA CTG TTA GTC Leu Lys Ser Ala Cys Asn Leu Ile Ala Leu Ile Leu Ile Leu Val 60 65 70	663
509 510	CAT AAG ATA TCC GCA GCT GGT AAC TTC GAG CTG GAA ATA TTA GAA ATC	711

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511 512 513	His 75	Lys	Ile	Ser	Ala	Ala 80	Gly	Asn	Phe	Glu	Leu 85	Glu	Ile	Leu	Glu	Ile 90	
514 515 516 517						CAT His											759
518 519 520 521						ACC Thr											807
522 523 524 525	_					CTG Leu											855
526 527 528 529						TGT Cys											903
530 531 532 533						GTG Val 160											951
534 535 536 537						CGT Arg											999
538 539 540 541						AAC Asn											1047
542 543 544 545						TCG Ser											1095
546 547 548 549	_					GGG Gly											1143
550 551 552 553						ACC Thr 240											1191
554 555 556 557						CAG Gln											1239
557 558 559 560 561						AAT Asn											1287

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562 563 564 565					GGC Gly												1320
566 567	(2)	INF	ORMA'	TION	FOR	SEQ	ID 1	NO:4	:								
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578	Met	Phe	Arg	Lys	His	Phe	Arg	Arg	Lys	Pro	Ala	Thr	Ser	Ser	Ser	Leu	
579	1				5					10					15		
580 581	Cl 11	Sar	Thr	Tla	Glu	Sar	ח ה	Λαn	cor	T 011	C1	Mot	cor	Tara	Tara	Th x	
582	Giu	261	1111	20	GIU	261	мта	Asp	25	пец	СТУ	MEL	261	30	цуѕ	1111	
583																	
584	Ala	Thr		Arg	Gln	Arg	Pro		His	Arg	Val	Pro	_	Ile	Ala	Thr	
585 586			35					40					45				
587	Len	Pro	Ser	Thr	Ile	Ara	Asp	Cvs	Δra	Ser	T ₁ e11	Lvg	Ser	Δla	Cvs	Δen	
588		50					55	Cyb	1129	501	Lou	60	501		Cyb	Abii	
589																	
590		Ile	Ala	Leu	Ile		Ile	Leu	Leu	Val		Lys	Ile	Ser	Ala		
591 592	65					70					75					80	
593	Gly	Asn	Phe	Glu	Leu	Glu	Ile	Leu	Glu	Ile	Ser	Asn	Thr	Asn	Ser	His	
594	-				85					90					95		
595	T	.	3	~1		a	~	~1	N L	D	27 -	~1				m\	
596 597	Leu	Leu	Asn	100	Tyr	Cys	Cys	GIY	мет 105	Pro	Ата	GIU	Leu	Arg	Ата	Tnr	
598									100								
599	Lys	Thr	Ile	Gly	Cys	Ser	Pro	Cys	Thr	Thr	Ala	Phe	Arg	Leu	Cys	Leu	
600			115					120					125				
601 602	Lvs	Glu	Tvr	Gln	Thr	Thr	Glu	Gln	Glv	Δla	Ser	Tle	Ser	Thr	Glv	Cvs	
603	-10	130	-1-	0111			135		017		501	140	501		017	070	
604																	
605		Phe	Gly	Asn	Ala		Thr	Lys	Ile	Leu	_	Gly	Ser	Ser	Phe		
606 607	145					150					155					160	
608	Leu	Ser	Asp	Pro	Gly	Val	Gly	Ala	Ile	Val	Leu	Pro	Phe	Thr	Phe	Arg	
609					165					170					175		
610 611	Тхх	ሞb v	Luc	Ser	Phe	Thr	Leu	Tla	Len	Gl n	Δ Ι ¬	T.e.r	Δαν	Met	Т 1122	7.00	
612	ııp	1111	Буз	180	FIIG	T11T	Leu	TT6	185	GIII	TTQ	בע	Top	190	TYL	Mali	

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613																	
614	Thr Ser Tyr Pro Asp Ala Glu Arg Leu Ile Glu Glu Thr Ser Tyr Ser 195 200 205 Gly Val Ile Leu Pro Ser Pro Glu Trp Lys Thr Leu Asp His Ile Gly 210 215 220 Arg Asn Ala Arg Ile Thr Tyr Arg Val Arg Val Gln Cys Ala Val Thr 225 240 Tyr Tyr Asn Thr Thr Cys Thr Thr Phe Cys Arg Pro Arg Asp Asp Gln 240 Tyr Tyr Asn Thr Thr Cys Gly Ser Glu Gly Gln Lys Leu Cys Leu Asn 260 270 Gly Trp Gln Gly Val Asn Cys Glu Glu Ala Ile Cys Lys Ala Gly Cys 275 280 Asp Pro Val His Gly 290 (2) INFORMATION FOR SEQ ID NO:5: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 267 base pairs (B) TypE: nucleic acid (C) STRANDEDMESS: double (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: CDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5: CGGTGGACTT CCTTCGTGTA TTGGTGGGAG CCCCCCCT AGGGGTCGGA GTCAGGTGGA 120																
615			195					200					205		-		
616	G1 1		T1_	T	D	0	D	~1		.	m1		_			~ J	
617 618			тте	Leu	Pro	ser		GIU	Trp	Lys	Thr		Asp	Hıs	IIe	GIY	
619	•	210					213					220					•
620	Arg A	Asn	Ala	Ara	Ile	Thr	Tvr	Ara	Val	Ara	Val	Gln	Cvs	Ala	Val	Thr	
621				3			-1-	9		9			CID		val		
622																	
623	Tyr 7	Гуr	Asn	Thr	Thr	Cys	Thr	Thr	Phe	Cys	Arg	Pro	Arg	Asp	Asp	Gln	
624					245					250					255		
625				_			-										
626	Phe (GLy	His		Ala	Cys	Gly	Ser		Gly	Gln	Lys	Leu	_	Leu	Asn	
627 628				260					265					270			
629	275 280 285 Asp Pro Val His Gly																
630	275 280 285 Asp Pro Val His Gly																
631	275 280 285 Asp Pro Val His Gly 290																
632	Asp Pro Val His Gly 290																
633	290																
634	290																
635	290 (2) INFORMATION FOR SEQ ID NO:5:																
636 637	290 (2) INFORMATION FOR SEQ ID NO:5: (i) SEQUENCE CHARACTERISTICS:																
638	290 (2) INFORMATION FOR SEQ ID NO:5: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 267 base pairs																
639	290 (2) INFORMATION FOR SEQ ID NO:5: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 267 base pairs (B) TYPE: nucleic acid																
640	(2) INFORMATION FOR SEQ ID NO:5: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 267 base pairs (B) TYPE: nucleic acid																
641																	
642			(I) T(POLO	GY:	unkr	nown									
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644	1	(ii)	MOI	ECUI	E T	PE:	cDN?	Ą									
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646 647																	
648		(xi)	SEC	HENC	e De	SCRI	грттс	OM ·	SEO T	א מ) - 5 -						
649		(,	22,	202211					v								
650	CGGT	GGAC	TT C	CTTC	GTG	TA T	rggTo	GGA	CCC	CTCGC	GAA	CGGC	GGG1	'AA (CACTO	BAAAGG	60
651																	
652	TCGAC	GTAC	CC F	ATTTC	CCGT	CA TA	AACGO	GTT	GTO	CGCCC	CCCT	AGG	GTCC	GA (STCAC	GTGGA	120
653																	
654	CGGG	AGGT	'CG I	CAAC	CGCCC	CG GC	GGA(:GGG	r GG7	raca:	rggt	GTAZ	AGGT	TT T	racco	GACCG	180
655 656	CCCN	N N CC	יממ יי	ים זים	المصمة	. n n -	ימממי	מ מייטח	, ,,,,,,	חש א מים	מא ממ	aaar	naama	acm o	7000	TCCAT	240
657	GGCAA	HLG	נ טטי	.CACA	10001	A AC		LGAA	. GG.	LAAC	LACG	GGG.	LCGTC		عدردر	FICCAT	240
658	CGAGT	rctg	GT Z	AGAC	GGTC	G C	CTTAZ	4G									267
659			•					_									
660	(2)	INFO	RMAI	CION	FOR	SEQ	ID 1	10:6	;								
661																	
662		(i)	_	-	CE CH												
663			(Z	A) LE	ENGTI	I: 57	74 ba	ase p	pairs	3							

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664 665 666 667 668 669	(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA	
670 671 672 673	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
674 675	GAATTCCTTC CATTATACGT GACTTTTCTG AAACTGTAGC CACCCTAGTG TCTCTAACTC	60
676 677	CCTCTGGAGT TTGTCAGCTT TGGTCTTTTC AAAGAGCAGG CTCTCTTCAA GCTCCTTAAT	120
678 679	GCGGGCATGC TCCAGTTTGG TCTGCGTCTC AAGATCACCT TTGGTAATTG ATTCTTCTTC	180
680 681	AACCCGGAAC TGAAGGCTGG CTCTCACCCT CTAGGCAGAG CAGGAATTCC GAGGTGGATG	240
682 683	TGTTAGATGT GAATGTCCGT GGCCCAGATG GCTGCACCCC ATTGATGTTG GCTTCTCCC	300
684		
685 686	GAGGAGGCAG CTCAGATTTG AGTGATGAAG ATGAAGATGC AGAGGACTGT TCTGCTAACA	360
687 688	TCATCACAGA CTTGGTCTAC CAGGGTGCCA GCCTCCAGNC CAGACAGACC GGACTGGTGA	420
689	GATGGCCCTG CACCTTGCAG CCCGCTACTC ACGGGCTGAT GCTGCCAAGC GTCTCCTGGA	480
690 691	TGCAGGTGCA GATGCCAATG CCCAGGACAA CATGGGCCGC TGTCCACTCC ATGCTGCAGT	540
692 693	GGCACGTGAT GCCAAGGTGT ATTCAGATCT GTTA	574
694		3,1
695 696	(2) INFORMATION FOR SEQ ID NO:7:	
697 698	(i) SEQUENCE CHARACTERISTICS:	
699	(A) LENGTH: 295 base pairs (B) TYPE: nucleic acid	
700	(C) STRANDEDNESS: double	
701 702	(D) TOPOLOGY: unknown	
703	(ii) MOLECULE TYPE: cDNA	
70 4 705		
706 707	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
707	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:/:	
709 710	TCCAGATTCT GATTCGCAAC CGAGTAACTG ATCTAGATGC CAGGATGAAT GATGGTACTA	60
711	CACCCTGAT CCTGGCTGCC CGCCTGGCTG TGGAGGGAAT GGTGGCAGAA CTGATCAACT	120
712 713 714	GCCAAGCGGA TGTGAATGCA GTGGATGACC ATGGAAAATC TGCTCTTCAC TGGGCAGCTG	180

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715	CTGTCAATAA TGTGGAGGCA ACTCTTTTGT TGTTGAAAAA TGGGGCCAAC CGAGACATGC	240
716 717	AGGACAACAA GGAAGAGACA CCTCTGTTTC TTGCTGCCCG GGAGGAGCTA TAAGC	205
718	AGGACAACAA GGAAGAGACA CCICIGIIIC IIGCIGCCCG GGAGGAGCIA IAAGC	295
719		
720	(2) INFORMATION FOR SEQ ID NO:8:	
721 722	(i) CECHENCE CHADACTEDICTICS.	
723	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 248 base pairs	
724	(B) TYPE: nucleic acid	
725	(C) STRANDEDNESS: double	
726	(D) TOPOLOGY: unknown	
727 728	(44) MOLEGILE WADE -DAY	
728 729	(ii) MOLECULE TYPE: cDNA	
730		
731		
732	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
733		
734 735	GAATTCCATT CAGGAGGAAA GGGTGGGGAG AGAAGCAGGC ACCCACTTTC CCGTGGCTGG	60
736	ACTCGTTCCC AGGTGGCTCC ACCGGCAGCT GTGACCGCCG CAGGTGGGGG CGGAGTGCCA	120
737	noted to the first	120
738	TTCAGAAAAT TCCAGAAAAG CCCTACCCCA ACTCGGACGG CAACGTCACA CCCGTGGGTA	180
739		
740	GCAACTGGCA CACAAACAGC CAGCGTGTCT GGGGCACGGG GGGATGGCAC CCCCTGCAGG	240
741 742	CAGAGCTG	248
743	CAGAGCIG	240
744	(2) INFORMATION FOR SEQ ID NO:9:	
745		
746	(i) SEQUENCE CHARACTERISTICS:	
747	(A) LENGTH: 323 base pairs	
748 749	(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
750	(D) TOPOLOGY: unknown	
751		
752	(ii) MOLECULE TYPE: cDNA	
753		
754 755		
756		
757	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
758		
759	TACGTATCTC GAGCACAGAC AGCTGACGTA CACTTTTNNA GTGCGAGGGA CATTCGTCCG	60
760 761		120
761 762	ACCAGTACGA ACATTTAGGC TCAGTACGGT AGGTCCATGG CCAAGACTAG GAGACGTAGG	120
763	GAGCTACAGG TCCCGCTCGC TAAACTCGGA CCACTGAAAC CTCCGGTCGA CAGTCGGTAA	180
764		
765	GCGAACAAGA GGGCCAGATC TTAGAGAAGG TGTCGCGGCG AGACTCGGGC TCGGGTCAGG	240

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766 767	CGG	CCTT	AAG (GACG'	rcgg	GC C	CNNN	AGGT(G AT	CAAG	ATCT	CGN	CNCG	GCG (GGCG	CCACC	т 300
768	aan.	~~~~	~~~														
769 770	CGA	3GNC(GAA 1	AACA	AGGG	AA A'	ľC										323
771																	
772	(2)	INF	'AMAC	rion	FOR	SEQ	ID I	1:00	0:								
773 774		/ i ') SEC	OTTENI	ים מי	יעםעה	יסיבייםי	T C TT T	~c.								
775		(-		-	ENGT					rs							
776					YPE:				_								
777			•		ranı				ble								
778 779			(1	D) 'I'	OPOLO	OGY:	unki	nown									
780		(ii) MOI	LECU	LE T	YPE:	cDN	A									
781		,															
782																	
783		(ix) FE				a Da										
784 785					AME/I CAT:			3234									
786			\'-	J, L	JCM1.		±	JZJ4									
787																	
788		(xi)) SE	QUEN	CE DI	ESCR	IPTI	ON: S	SEQ :	ID N	0:10	:					
789 790	maa.	C T C	GAG	an a	aaa	aaa	777	770	ama	maa	700	ama	a a	шаа	7 7 7	770	4.0
790 791			Glu														48
792	1	0		1100	5	O±1	11011	_,	***	10	50-	200	0111	Cyb	15	Abii	
793																	
794			TGC														96
795 796	His	Ala	Cys	G1y 20	Trp	Asp	GIY	GTA	Asp 25	Cys	Ser	Leu	Asn	Phe 30	Asn	Asp	
797				20					25					30			
798	CCC	TGG	AAG	AAC	TGC	ACG	CAG	TCT	CTG	CAG	TGC	TGG	AAG	TAC	TTC	AGT	144
799	Pro	Trp	Lys	Asn	Cys	Thr	Gln		Leu	Gln	Cys	Trp	_	\mathtt{Tyr}	Phe	Ser	
800 801			35					40					45				
801	GAC	GGC	CAC	тст	GAC	AGC	CAG	TGC	AAC	тсъ	GCC	GGC	TGC	СТС	ጥጥር	GAC	192
803			His														
804		50					55					60	_			_	
805	~~~		~~~	= 00	~~~		~~~	~~~	~~~	~-~		~	~~~	~~~		~~~	0.10
806 807			GAC Asp														240
808	65	FIIC	Asp	СуБ	GIII	70	ALG	Gru	Gry	GLII	75	ASII	FIO	пец	ı yı	80	
809																	
810			TGC														288
811	Gln	Tyr	Cys	Lys	_	His	Phe	Ser	Asp	_	His	Cys	Asp	Gln	_	Cys	
812 813					85					90					95		
814	AAC	AGC	GCG	GAG	TGC	GAG	TGG	GAC	GGG	CTG	GAC	TGT	GCG	GAG	CAT	GTA	336
815			Ala	Glu					Gly					Glu			
816				100					105					110			

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817 818 819 820			GCC Ala						384
821 822 823 824			AAC Asn						432
825 826 827 828 829			AAC Asn 150				 	 	480
830 831 832 833			TAC Tyr						528
834 835 836 837			GCC Ala						576
838 839 840 841			TCG Ser						624
842 843 844 845			GAC Asp						672
846 847 848 849			CGG Arg 230						720
850 851 852 853			GTG Val						768
854 855 856 857			CCC Pro		_		 _	 	816
858 859 860 861			CCG Pro						864
862 863 864 865			CTG Leu						912
866 867			CAG Gln						960

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868 869	305					310					315					320		
870 871 872 873				GAG Glu													1	800.
874 875 876 877				GGC Gly 340													1	.056
878 879 880 881				AAC Asn	_												1	.104
882 883 884 885				TTC Phe													1	.152
886 887 888 889				CGG Arg													1	.200
890 891 892 893				GCC Ala													1	.248
894 895 896 897				GAC Asp 420													1	.296
898 899 900 901				TCC Ser													1	.344
902 903 904 905				GAC Asp													1	.392
906 907 908 909				CAC His													1	440
910 911 912 913				CGC Arg													1	.488
914 915 916 917				GAT Asp 500													1	.536
918	CAT	GCG	GCT	GTG	TCT	GCC	GAC	GCA	CAA	GGT	GTC	TTC	CAG	ATC	CTG	ATC	1	584

RAW SEQUENCE LISTING PATENT APPLICATION US/08/083,590

DATE: 12/16/93 TIME: 13:09:40

INPUT SET: S7068.raw

919 920 921	His	Ala	Ala 515	Val	Ser	Ala	Asp	Ala 520	Gln	Gly	Val	Phe	Gln 525	Ile	Leu	Ile	
922 923 924 925						GAC Asp											1632
926 927 928 929						GCC Ala 550											1680
930 931 932 933						GCC Ala											1728
934 935 936 937						GCC Ala											1776
938 939 940 941						GGG Gly											1824
942 943 944 945						CTG Leu											1872
946 947 948 949						CAC His 630											1920
950 951 952 953						GAC Asp											1968
954 955 956 957	_					GAG Glu											2016
958 959 960 961						GGC Gly											2064
962 963 964						GGC Gly											2112
965 966 967 968 969						AGC Ser 710											2160

RAW SEQUENCE LISTING PATENT APPLICATION US/08/083,590

INPUT SET: S7068.raw

DATE: 12/16/93 TIME: 13:09:46

970 971 972 973	GAC Asp									2208
974 975 976 977	CTG Leu									2256
978 979 980 981	CAT His	_				_	 	 	 	2304
982 983 984 985	TTC Phe 770									2352
986 987 988 989	GAC Asp									2400
990 991 992 993	ATG Met									2448
994 995 996 997	CCT Pro									2496
998 999 1000 1001	GGC Gly									2544
1002 1003 1004 1005	AGT Ser 850									2592
1006 1007 1008 1009	GTG Val									2640
1010 1011 1012 1013	CTG Leu									2688
1014 1015 1016 1017	CAC His									2736
1018 1019 1020	GGC Gly		 	 	 					2784

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INPUT SET: S7068.raw

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1021																		
1022		CAG															28:	32
1023	Thr	Gln	Gln	Val	Gln	Pro		Asn	Leu	Gln	Met		Gln	Gln	Asn	Leu		
1024		930					935					940						
1025																		
1026	_	CCA															28	80
1027	Gln	Pro	Ala	Asn	Ile	Gln	Gln	Gln	Gln	Ser	Leu	Gln	Pro	Pro	Pro	Pro		
1028	945					950					955					960		
1029																		
1030		CCA															29:	28
1031	Pro	Pro	Gln	Pro	His	Leu	${ t Gly}$	Val	Ser	Ser	Ala	Ala	Ser	Gly	His	Leu		
1032					965					970					975			
1033																		
1034		CGG															29'	76
1035	Gly	Arg	Ser	Phe	Leu	Ser	Gly	Glu	Pro	Ser	Gln	Ala	Asp	Val	Gln	Pro		
1036				980					985					990				
1037																		
1038	CTG	GGC	CCC	AGC	AGC	CTG	GCG	GTG	CAC	ACT	ATT	CTG	CCC	CAG	GAG	AGC	302	24
1039	Leu	Gly	Pro	Ser	Ser	Leu	Ala	Val	His	Thr	Ile	Leu	Pro	Gln	Glu	Ser		
1040			995					1000)				100	5				
1041																		
1042	CCC	GCC	CTG	CCC	ACG	TCG	CTG	CCA	TCC	TCG	CTG	GTC	CCA	CCC	GTG	ACC	30	72
1043	Pro	Ala	Leu	Pro	Thr	Ser	Leu	Pro	Ser	Ser	Leu	Val	Pro	Pro	Val	Thr		
1044		1010)				1015	5				1020	כ					
1045																		
1046	GCA	GCC	CAG	TTC	CTG	ACG	CCC	CCC	TCG	CAG	CAC	AGC	TAC	TCC	TCG	CCT	312	20
1047	Ala	Ala	Gln	Phe	Leu	Thr	Pro	Pro	Ser	Gln	His	Ser	Tyr	Ser	Ser	Pro		
1048	102	5				1030	כ				103	5				1040		
1049																		
1050	GTG	GAC	AAC	ACC	CCC	AGC	CAC	CAG	CTA	CAG	GTG	CCT	GTT	CCT	GTA	ATG	316	68
1051	Val	Asp	Asn	Thr	Pro	Ser	His	Gln	Leu	Gln	Val	Pro	Val	Pro	Val	Met		
1052					1045	5				1050)				105	5		
1053																		
1054		ATG															32:	16
1055	Val	Met	Ile	_		Ser	Asp	Pro	Ser	Lys	Gly	Ser	Ser	Ile	Leu	Ile		
1056				1060)				1069	5				1070)			
1057																		
1058		GCT															323	34
1059	GLu	Ala			Ser	Trp												
1060			1075	5														
1061																		
1062	>																	
1063	(2)	INF	ORMA'	rion	FOR	SEQ	ID 1	NO:11	L:									
1064			, , ,															
1065			(1) 5	SEQUE														
1066					LEI					acio	is							
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1071																		

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1072		(:	xi) s	SEQUI	ENCE	DES	CRIP	rion	: SE	Q ID	NO:	11:				
1073 1074 1075 1076	Cys 1	Gln	Glu	Asp	Ala 5	Gly	Asn	Lys	Val	Cys 10	Ser	Leu	Gln	Cys	Asn 15	Asn
1077 1078 1079	His	Ala	Cys	Gly 20	Trp	Asp	Gly	Gly	Asp 25	Cys	Ser	Leu	Asn	Phe 30	Asn	Asp
1080 1081 1082	Pro	Trp	Lys 35	Asn	Cys	Thr	Gln	Ser 40	Leu	Gln	Cys	Trp	Lys 45	Tyr	Phe	Ser
1083 1084 1085	Asp	Gly 50	His	Cys	Asp	Ser	Gln 55	Cys	Asn _.	Ser	Ala	Gly 60	Cys	Leu	Phe	Asp
1086 1087 1088	65				Gln	70					75					80
1089 1090 1091			_	_	Asp 85				_	90		-	-		95	-
1092 1093 1094				100	Cys			_	105		_	_		110		
1095 1096 1097			115		Ala		_	120					125			
1098 1099 1100		130			Arg		135					140				
1101 1102 1103	145				Thr	150				-	155	_			Ī	160
1104 1105 1106					Pro 165		_	_		170				_	175	
1107 1108 1109				180	Ala				185					190		
1110 1111 1112	_		195		Ala _			200		_	_		205		_	_
1113 1114 1115		210	_		Leu		215					220				<u>-</u>
1116 1117 1118	225				Asn	230					235					240
1119 1120 1121					Asp 245					250	_				255	
1122	Gly	Ser	Leu	Asn	Ile	Pro	Tyr	Lys	Ile	Glu	Ala	Val	Gln	Ser	Glu	Thr

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1123				260					265					270		
1124																
1125	Val	Glu	Pro	Pro	Pro	Pro	Ala	Gln	Leu	His	Phe	Met	Tyr	Val	Ala	Ala
1126			275					280					285			
1127																
1128	Ala	Ala	Phe	Val	Leu	Leu	Phe	Phe	Val	Gly	Cys	Gly	Val	Leu	Leu	Ser
1129		290					295					300				
1130																
1131	Arg	Lys	Arg	Arg	Arg	Gln	His	Gly	Gln	Leu	${\tt Trp}$	Phe	Pro	Glu	Gly	Phe
1132	305					310					315					320
1133																
1134	Lys	Val	Ser	Glu	Ala	Ser	Lys	Lys	Lys	Arg	Arg	Glu	Pro	Leu	Gly	Glu
1135					325					330					335	
1136																
1137	Asp	Ser	Val	Gly	Leu	Lys	Pro	Leu	Lys	Asn	Ala	Ser	Asp	Gly	Ala	Leu
1138				340					345					350		
1139																
1140	Met	Asp	_	Asn	Gln	Asn	Glu	${\tt Trp}$	Gly	Asp	Glu	Asp	Leu	Glu	Thr	Lys
1141			355					360					365			
1142																
1143	Lys		Arg	Phe	Glu	Glu	Pro	Val	Val	Leu	Pro	Asp	Leu	Asp	Asp	Gln
1144		370					375					380				
1145																
1146		Asp	His	Arg	Gln	${\tt Trp}$	Thr	Gln	Gln	His	Leu	Asp	Ala	Ala	Asp	Leu
1147	385					.390					395					400
1148				_		_										
1149	Arg	Met	Ser	Ala	Met	Ala	Pro	Thr	Pro	Pro	Gln	Gly	Glu	Val	Asp	Ala
1150					405					410					415	
1151																
1152	Asp	Cys	Met		Val	Asn	Val	Arg		Pro	Asp	Gly	Phe		Pro	Leu
1153				420					425	,				430		
1154				_	_	_				_					_	_
1155	Met	IIe		Ser	Cys	Ser	GIŸ		GТУ	Leu	Glu	Thr		Asn	Ser	Glu
1156			435					440					445			
1157	~1	a 1	a 1	7		D	- I	•• •	-1	_	_	D 1	-1	_	~1	~ 7
1158 `	GIU		GIU	Asp	Ala	Pro		vaı	тте	ser	Asp		тте	Tyr	GIn	GLY
1159		450					455					460				
1160	77.	C	T	774 -	7	a1	mla aa	7	7	ml	a1	a1	ml	77-	T	TT -
1161		ser	ьeu	HIS	Asn		Inr	Asp	Arg	THE	-	GIU	Inr	Ата	ьeu	
1162 1163	465					470					475					480
1164	T 011	777	71.	7 200	Пт гэс	C 0 20	7 200	C0.20	7.00	71.	71.	T	7 200	T 011	T 011	a 1
1165	пеп	AIA	Ата	Arg	Tyr 485	261	Arg	261	Asp	490	нта	пур	Arg	пеп		GIU
1166					403					430					495	
1167	Δl -	202	λ] -	7/ 02	Ala	7 cr	Tla	al n	7	Ner	Mo+	<u> </u>	7 ~~	Th∽	Dro	Ten
1168	лта	SET	лта	500	лта	POII	116	GTII	505	Pall	MEC	GTÅ	Ary		FIO	шeи
1169				500					203					510		
1170	Hic	Δls	Δls	Va 1	Ser	Δls	Agn	Δls	Gln	Gl v	1721	Dhe	Gln	T۱۵	Leu	т1Б
1171	****	AT CL	515	v ca ±	DCI	n_a	rah	520	0111	СТУ	val	F 11G	525	116	Leu	TTC
1172			J _ J					J2 (223			
1173	Ara	Asn	Ara	Δla	Thr	Agn	Leu	Agn	Δla	Δrσ	Met	Hic	Agn	Glv	Thr	Thr
,	9		9			- 12 P	u	Top	A_G	9	1-10-0	****3	Tob	O-Y	T 11 T	T 11T

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1174		530					535					540				
1175 1176	Pro	Leu	Tle	Leu	Δla	Δla	Ara	Leu	Δla	Val	Glu	Glv	Met	T.e.11	Glu	Δen
1177	545	Lou		шоц		550		шоц	1114		555	017		пси	O_u	560
1178																
1179	Leu	Ile	Asn	Ser	His	Ala	Asp	Val	Asn	Ala	Val	Asp	Asp	Leu	Gly	Lys
1180					565		_			570		_	_		575	•
1181																
1182	Ser	Ala	Leu	His	${\tt Trp}$	Ala	Ala	Ala	Val	Asn	Asn	Val	Asp	Ala	Ala	Val
1183				580					585					590		
1184						_	_									
1185	Val	Leu		Lys	Asn	Gly	Ala		Lys	Asp	Met	Gln		Asn	Arg	Glu
1186			595					600					605			
1187		1	_	_	_,	_			_		~-7	_	_			
1188	GIu	Thr	Pro	Leu	Phe	Leu		Ala	Arg	Glu	GТУ		Tyr	Glu	Thr	Ala
1189		610					615					620				
1190 1191	Tara	Val	T 011	T 011	7 an	uic	Dho	ת [ת	7 cm	7 ~~	7 an	T10	Thr	7 an	uic	Mot
1192	625	vai	цец	пеп	Asp	630	PHE	AIA	ASII	Arg	635	TIE	TIII	ASP	птъ	640
1193	023					0.50					033					040
1194	Asp	Arg	Leu	Pro	Ara	Asp	Tle	Ala	Gln	Glu	Ara	Met	His	His	Asn	Tle
1195	115p		ДСЦ		645	пор		1114	0111	650	m-9	1100	1110	1115	655	110
1196																
1197	Val	Arg	Leu	Leu	Asp	Glu	Tyr	Asn	Leu	Val	Arq	Ser	Pro	Gln	Leu	His
1198		-		660	_		•		665		J			670		
1199																
1200	Gly	Ala	Pro	Leu	Gly	Gly	Thr	Pro	Thr	Leu	Ser	Pro	Pro	Leu	Cys	Ser
1201			675					680					685		_	
1202																
1203	Pro	Asn	Gly	Tyr	Leu	Gly	Ser	Leu	Lys	Pro	Gly	Val	Gln	Gly	Lys	Lys
1204		690					695					700				
1205	_							_		_					_	_
1206		Arg	Lys	Pro	Ser		Lys	GLY	Leu	Ala	_	Gly	Ser	Lys	Glu	
1207	705					710					715					720
1208 1209	T	7 an	T 011	T	77.	7 200	7 20 00	T	T	C 0.20	<u>ما -</u>	7	a1	T	<u>ما</u>	O
1210	ьуѕ	Asp	ьeu	гуѕ	725	Arg	Arg	гуѕ	гуѕ	730	GIII	Asp	GIY	гуѕ	735	Cys
1211					125					/30					133	
1212	Leu	Leu	Agn	Ser	Ser	Glv	Met	Len	Ser	Pro	Val	Asp	Ser	T.e.11	Glu	Ser
1213		Lou		740	501	0-7		Lou	745		• • • •	1155	501	750	014	501
1214				•												
1215	Pro	His	Glv	Tvr	Leu	Ser	Asp	Val	Ala	Ser	Pro	Pro	Leu	Leu	Pro	Ser
1216			755	•			-	760					765	_		
1217																
1218	Pro	Phe	Gln	Gln	Ser	${\tt Pro}$	Ser	Val	Pro	Leu	Asn	His	Leu	Pro	Gly	Met
1219		770					775					780				
1220																
1221		Asp	Thr	His	Leu	-	Ile	Gly	His	Leu		Val	Ala	Ala	Lys	
1222	785					790					795					800
1223	~ 3				_	~ 7	~ ?	~ 7	~ 7	_	_		-1	~ 7	1	~1
1224	Glu	Met	Ala	Ala	Leu	GIY	GLY	GТУ	GLY	Arg	Leu	Ala	Phe	GLu	Thr	Gly

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1225 1226					805					810					815	
1227 1228 1229	Pro	Pro	Arg	Leu 820	Ser	His	Leu	Pro	Val 825	Ala	Ser	Gly	Thr	Ser 830	Thr	Val
1230 1231 1232	Leu	Gly	Ser 835	Ser	Ser	Gly	Gly	Ala 840	Leu	Asn	Phe	Thr	Val 845	Gly	Gly	Ser
1233 1234 1235	Thr	Ser 850	Leu	Asn	Gly	Gln	Cys 855	Glu	Trp	Leu	Ser	Arg 860	Leu	Gln	Ser	Gly
1236 1237 1238	Met 865	Val	Pro	Asn	Gln	Tyr 870	Asn	Pro	Leu	Arg	Gly 875	Ser	Val	Ala	Pro	Gly 880
1239 1240 1241	Pro	Leu	ser	Thr	Gln 885	Ala	Pro	Ser	Leu	Gln 890	His	Gly	Met	Val	Gly 895	Pro
1242 1243 1244	Leu	His	Ser	Ser 900	Leu	Ala	Ala	Ser	Ala 905	Leu	Ser	Gln	Met	Met 910	Ser	Tyr
1245 1246 1247	Gln	Gly	Leu 915	Pro	Ser	Thr	Arg	Leu 920	Ala	Thr	Gln	Pro	His 925	Leu	Val	Gln
1248 1249 1250	Thr	Gln 930	Gln	Val	Gln	Pro	Gln 935	Asn	Leu	Gln	Met	Gln 940	Gln	Gln	Asn	Leu
1251 1252 1253	Gln 945	Pro	Ala	Asn	Ile	Gln 950	Gln	Gln	Gln	Ser	Leu 955	Gln	Pro	Pro	Pro	Pro 960
1254 1255 1256	Pro	Pro	Gln	Pro	His 965	Leu	Gly	Val	Ser	Ser 970	Ala	Ala	Ser	Gly	His 975	Leu
1257 1258 1259	Gly	Arg	Ser	Phe 980	Leu	Ser	Gly	Glu	Pro 985	Ser	Gln	Ala	Asp	Val 990	Gln	Pro
1260 1261 1262	Leu	Gly	Pro 995	Ser	Ser	Leu	Ala	Val 1000		Thr	Ile	Leu	Pro 1009		Glu	Ser
1263 1264 1265	Pro	Ala 1010		Pro	Thr	Ser	Leu 101		Ser	Ser	Leu	Val 1020		Pro	Val	Thr
1266 1267 1268	Ala 102		Gln	Phe	Leu	Thr 1030		Pro	Ser	Gln	His 1035		Tyr	Ser	Ser	Pro 1040
1269 1270 1271	Val	Asp	Asn	Thr	Pro 1045		His	Gln	Leu	Gln 105		Pro	Val	Pro	Val 105	
1272 1273 1274	Val	Met	Ile	Arg 1060		Ser	Asp	Pro	Ser 1065	_	Gly	Ser	Ser	Ile 1070		Ile
1275	Glu	Ala	Pro	Asp	Ser	Trp										

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(2) INFORMATION FOR SEQ ID NO:12: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 4268 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 2..1972 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: G GAG GTG GAT GTG TTA GAT GTG AAT GTC CGT GGC CCA GAT GGC TGC Glu Val Asp Val Leu Asp Val Asn Val Arg Gly Pro Asp Gly Cys ACC CCA TTG ATG TTG GCT TCT CTC CGA GGA GGC AGC TCA GAT TTG AGT Thr Pro Leu Met Leu Ala Ser Leu Arg Gly Gly Ser Ser Asp Leu Ser GAT GAA GAT GAA GAT GCA GAG GAC TCT TCT GCT AAC ATC ATC ACA GAC Asp Glu Asp Glu Asp Ala Glu Asp Ser Ser Ala Asn Ile Ile Thr Asp TTG GTC TAC CAG GGT GCC AGC CTC CAG GCC CAG ACA GAC CGG ACT GGT Leu Val Tyr Gln Gly Ala Ser Leu Gln Ala Gln Thr Asp Arg Thr Gly GAG ATG GCC CTG CAC CTT GCA GCC CGC TAC TCA CGG GCT GAT GCT GCC Glu Met Ala Leu His Leu Ala Ala Arg Tyr Ser Arg Ala Asp Ala Ala AAG CGT CTC CTG GAT GCA GGT GCA GAT GCC CAG GAC AAC ATG Lys Arg Leu Leu Asp Ala Gly Ala Asp Ala Asn Ala Gln Asp Asn Met GGC CGC TGT CCA CTC CAT GCT GCA GTG GCA GCT GAT GCC CAA GGT GTC Gly Arg Cys Pro Leu His Ala Ala Val Ala Ala Asp Ala Gln Gly Val TTC CAG ATT CTG ATT CGC AAC CGA GTA ACT GAT CTA GAT GCC AGG ATG Phe Gln Ile Leu Ile Arg Asn Arg Val Thr Asp Leu Asp Ala Arg Met

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1327																	
1328	AAT	GAT	GGT	ACT	ACA	CCC	CTG	ATC	CTG	GCT	GCC	CGC	CTG	GCT	GTG	GAG	430
1329	Asn	Asp	Gly	Thr	Thr	Pro	Leu	Ile	Leu	Ala	Ala	Arg	Leu	Ala	Val	Glu	
1330			130					135					140				
1331																	
1332	GGA	ATG	GTG	GCA	GAA	CTG	ATC	AAC	TGC	CAA	GCG	GAT	GTG	AAT	GCA	GTG	478
1333				Ala													
1334	-	145					150		- 2			155					
1335																	
1336	GAT	GAC	CAT	GGA	AAA	тст	GCT	СТТ	CAC	TGG	GCA	GCT	GCT	GTC	ДДТ	Тαα	526
1337				Gly													3_3
1338	160			0-1	-10	165					170	1124	1124		11-11	175	
1339	100					100					1,0					1,75	
1340	стс	CAC	CCA	ACT	СТТ	ттс	ттс	ጥጥር	א א א	አአጥ	ccc	CCC	አአሮ	CCA	CAC	አጥር	574
1341																	3/4
1341	Val	Giu	Ата	Thr		пец	пец	цец	пуъ		GIY	Ата	ASII	Arg		Mec	
					180					185					190		
1343	a . a	a	770	770	C1 7 7	a 7 a	707	aam	ama.		CITIES .	a a m	000	000	a 3 a	aaa	622
1344				AAG													622
1345	GII	Asp	ASI	Lys	GIU	GIU	THE	Pro		Pne	ьeu	Ата	Ата	_	GIU	GIY	
1346				195					200					205			
1347			~	~~-	~~~			~=~		~~~			~~~		~~-	~-~	
1348				GCA													670
1349	Ser	Tyr		Ala	Ата	га	тте		ьeu	Asp	His	Pne	_	Asn	Arg	Asp	
1350			210					215					220				
1351																	
1352				CAT													718
1353	Ile		Asp	His	Met	Asp	_	Leu	Pro	Arg	Asp		Ala	Arg	Asp	Arg	
1354		225					230					235					
1355																	
1356				GAC													766
1357		His	His	Asp	Ile		Arg	Leu	Leu	Asp		Tyr	Asn	Val	Thr		
1358	240					245					250					255	
1359																	
1360				GGC													814
1361	Ser	Pro	Pro	Gly	Thr	Val	Leu	Thr	Ser		Leu	Ser	Pro	Val	Ile	Cys	
1362					260					265					270		
1363																	
1364	GGG	CCC	AAC	AGA	TCT	TTC	CTC	AGC	CTG	AAG	CAC	ACC	CCA	ATG	GGC	AAG	862
1365	Gly	Pro	Asn	Arg	Ser	Phe	Leu	Ser	Leu	Lys	His	Thr	Pro	Met	Gly	Lys	
1366				275					280					285			
1367																	
1368	AAG	TCT	AGA	CGG	CCC	AGT	GCC	AAG	AGT	ACC	ATG	CCT	ACT	AGC	CTC	CCT	910
1369	Lys	Ser	Arg	Arg	Pro	Ser	Ala	Lys	Ser	Thr	Met	Pro	Thr	Ser	Leu	Pro	
1370			290					295					300				
1371																	
1372	AAC	CTT	GCC	AAG	GAG	GCA	AAG	GAT	GCC	AAG	GGT	AGT	AGG	AGG	AAG	AAG	958
1373				Lys													
1374		305		-			310	_		-	_	315	_	_	·		
1375																	
1376	TCT	CTG	AGT	GAG	AAG	GTC	CAA	CTG	TCT	GAG	AGT	TCA	GTA	ACT	TTA	TCC	1006
1377				Glu													
					-												

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													•				
1378 1379	320					325					330					335	
1380	CCT	GTT	GAT	TCC	CTA	GAA	TCT	CCT	CAC	ACG	TAT	GTT	TCC	GAC	ACC	ACA	1054
1381		Val															1001
1382			_		340					345	•			-	350		
1383																	
1384		TCT															1102
1385 1386	Ser	Ser	Pro		Ile	Thr	Ser	Pro	_	Ile	Leu	GIn	Ala		Pro	Asn	
1387				355					360					365			
1388	CCT	ATG	TTG	GCC	ACT	GCC	GCC	CCT	CCT	GCC	CCA	GTC	CAT	GCC	CAG	CAT	1150
1389		Met															
1390			370					375					380				
1391																	
1392		CTA															1198
1393 1394	Ala	Leu 385	ser	Pne	ser	ASII	390	HIS	GIU	мес	GIN	395	Leu	Ата	HIS	GIY	
1395		303					390					393					
1396	GCC	AGC	ACT	GTG	CTT	CCC	TCA	GTG	AGC	CAG	TTG	CTA	TCC	CAC	CAC	CAC	1246
1397	Ala	Ser	Thr	Val	Leu	Pro	Ser	Val	Ser	Gln	Leu	Leu	Ser	His	His	His	
1398	400					405					410					415	
1399	3 MM	аша	mam	a a z	aaa	3 Cm	~~	7 CI	a a m	aa .	300	mma	3 Cm	3.00	ama.	G 3 TF	1004
1400 1401		GTG Val															1294
1402	110	vai	Ser	FIO	420	Ser	СТУ	261	Ата	425	261	пец	261	Arg	430	nis	
1403																	
1404	CCA	GTC	CCA	GTC	CCA	GCA	GAT	TGG	ATG	AAC	CGC	ATG	GAG	GTG	AAT	GAG	1342
1405	Pro	Val	Pro	Val	Pro	Ala	Asp	Trp	Met	Asn	Arg	Met	Glu	Val	Asn	Glu	
1406				435					440					445			
1407 1408	7 00	C A C	TIN CI	7 7 TT	C T C	7 mG	mmm	ССШ	7 ma	ama	ama	ССТ	aa z	COM	a 7 a	aaa	1200
1408		CAG Gln															1390
1410		0111	450	11011	014		1110	455	1100	vai	LCu	AIU	460	niu	Oru	Gry	
1411																	
1412		CAT															1438
1413	Thr	His	Pro	Gly	Ile	Ala		Gln	Ser	Arg	Pro		Glu	Gly	Lys	His	
1414 1415		465					470					475					
1415	ΔΤΔ	ACC	ACC	ССТ	CGG	GAG	כככ	ጥጥር፡	כככ	כככ	ΔТТ	стс	ΔСТ	יייכ	CAG	CTC	1486
1417		Thr	_								_	_	_	_	_		1400
1418	480				J	485					490					495	
1419																	
1420		CCT															1534
1421	Ile	Pro	Lys	Gly		Ile	Ala	Gln	Pro	•	Gly	Ala	Pro	Gln		Gln	
1422 1423					500					505					510		
1423	TCC	ACC	TGC	ССТ	CCA	GCT	GTT	GCG	GGC	כככ	СТС	CCC	ACC	АТС	TAC	CAG	1582
1425		Thr															
1426			-	515					520					525	4		
1427																	
1428	ATT	CCA	GAA	ATG	GCC	CGT	TTG	CCC	AGT	GTG	GCT	TTC	CCC	ACT	GCC	ATG	1630

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1429	Ile	Pro	Glu	Met	Ala	Arg	Leu	Pro	Ser	Val	Ala	Phe	${\tt Pro}$	Thr	Ala	Met	
1430			530					535					540				
1431	3 ma	000	a	a	a	222	a	C/D3	a am	a	3.00	3 mm	ama		~~~		
1432 1433				CAG Gln													1678
1434	MEC	545	GIII	GIII	Asp	GIY	550	vai	ніа	GIII	1111	555	Leu	PIO	Ala	TYL	
1435		343					330					222					
1436	CAT	CCT	TTC	CCA	GCC	TCT	GTG	GGC	AAG	TAC	CCC	ACA	CCC	CCT	TCA	CAG	1726
1437				Pro													
1438	560					565		_	_	-	570					575	
1439																	
1440				GCT												_	1774
1441	His	Ser	Tyr	Ala		Ser	Asn	Ala	Ala		Arg	Thr	Pro	Ser		Ser	
1442					580					585					590		
1443 1444	COT	CAC	CTC	CAG	COT	CAC	CAT	aaa	T A C	OTT C	7 (7	CC7	TCC	CC7	CAC	TI CIT	1022
1444				Gln													1822
1446	Gry	1113	Бец	595	GIY	Giu	1113	FIO	600	пеп	1111	PIO	261	605	Giu	361	
1447				555					000					005			
1448	CCT	GAC	CAG	TGG	TCA	AGT	TCA	TCA	CCC	CAC	TCT	GCT	TCT	GAC	TGG	TCA	1870
1449	Pro	Asp	Gln	Trp	Ser	Ser	Ser	Ser	Pro	His	Ser	Ala	Ser	Asp	Trp	Ser	
1450			610					615					620		_		
1451																	
1452				ACC													1918
1453	Asp		Thr	Thr	Ser	Pro		Pro	Gly	Gly	Ala	_	Gly	Gly	Gln	Arg	
1454		625					630					635					
1455 1456	CCA	ССТ	GGG	ACA	CAC	λΤС	тст	C A C	CCN	CCA	CAC	አአሮ	አአሮ	አጥር	CAG	СТТ	1966
1457				Thr													1966
1458	640		O±,		*****	645	501	O-u	110	-10	650	11011	11011		0111	655	
1459																	
1460	TAT	GCG	TGAC	GAGA	GTC (CACC'	rcca(GT G	raga(GACA?	C AAC	CTGA	TTT	TGT	TAA	€CT	2022
1461	Tyr	Ala															
1462																	
1463																	
1464	GCT	BAGGA	AAC A	TAAA	SAAGO	FT C	ATCC	3GGA(3 AGA	YAAI	BAAG	AAA'	rctc.	rgg <i>I</i>	AGCC	AGCTTC	2082
1465 1466	ሞአ ር ፣	COTT	NCC 7	מי <i>ו</i> אר או	\	יים מי	יייייייייייייייייייייייייייייייייייייי	ריתי איתי	ר כאנ	י תידות ר	שממ	7701	\	י מסי	י שייי כי	STCAGT	2142
1467	IAGA	10011	A DUA	HAAGA	MADI	3A 1(31 I C.	LIAI.	L CAC	3A 1 AA	41.GC	AAGA	MADI	CAF	11100	FICAGI	2142
1468	TTC	CTGC	GT A	АТСТС	CAAC	ag Ci	TATT	rgati	r ATT	гстал	тст	AATA	AGA	'AA C	TTTT	TGGAA	2202
1469	0-	-0-0						. 0							,		
1470	ATG	CAAG	ATG A	ATAA	CAAG	CC T	rggg:	rcca:	r GT	TAC	CTC	TTC	CATT	rgg <i>i</i>	AGAA'	TAAGAT	2262
1471																	
1472	GGAT	GCT	TAT T	rgaa(3CCC2	AG AG	CATT	CTTG	CAG	CTTGC	ACT	GCA	CTTTZ	AAG (CCCT	SCAGGC	2322
1473																	
1474	TTCT	rGCC <i>I</i>	ATA 7	rcca:	I'GAGA	AA GA	ATTC:	L'ACA(CTAC	3CGT(CTG	TTG	3GAAT	TA 7	rGCC	CTGGAA	2382
1475 1476	The Co	ומממי	י איט	∖ mm∕i i	\	\C C	א חיים מי	ר כי כי די	7 (Jm/	ארוויירו	יכז כ	7 000	الماليات	rem e	دارساسات	ATTTGG	2442
1476	1101	.GCC.	LGA A	7110		G(AIC.		- (1(11	JAU	WII(-111		_ I I C#	111100	2442
1478	TGCT	TTTT	GT T	rttgo	CACC	rc To	CCGT	SATTO	TAC	3CCC1	CACC	AGC	ATGTT	TAT A	AGGG	CAAGAC	2502
1479									_					_		-	

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1480 1481	CTTTGTGCTT	TTGATCATTC	TGGCCCATGA	AAGCAACTTT	GGTCTCCTTT	CCCCTCCTGT	2562
1482	CTTCCCGGTA	TCCCTTGGAG	TCTCACAAGG	TTTACTTTGG	TATGGTTCTC	AGCACAAACC	2622
1483 1484	TTTCAAGTAT	GTTGTTTCTT	TGGAAAATGG	ACATACTGTA	TTGTGTTCTC	CTGCATATAT	2682
1485							
1486 1487	CATTCCTGGA	GAGAGAAGGG	GAGAAGAATA	CTTTTCTTCA	ACAAATTTTG	GGGGCAGGAG	2742
1488	ATCCCTTCAA	GAGGCTGCAC	CTTAATTTTT	CTTGTCTGTG	TGCAGGTCTT	CATATAAACT	2802
1489							
1490	TTACCAGGAA	${\tt GAAGGGTGTG}$	${\tt AGTTTGTTGT}$	${\tt TTTTCTGTGT}$	ATGGGCCTGG	TCAGTGTAAA	2862
1491							
1492	GTTTTATCCT	TGATAGTCTA	GTTACTATGA	CCCTCCCCAC	TTTTTTAAAA	CCAGAAAAAG	2922
1493	ammmaa		a	~~~~~	~~~~~~~	am aaaaa	
1494	GTTTTGGAATG	TTGGAATGAC	CAAGAGACAA	GTTAACTCGT	GCAAGAGCCA	GTTACCCACC	2982
1495 1496	CA CA COMOCO	COMA CIMITACIONI	acarraca mm	CCA TITICA CITIC	астата паса	3 G3 G3 III II I	2042
1496	CACAGGTCCC	CCTACTTCCT	GCCAAGCATT	CCATTGACTG	CCIGIAIGGA	ACACATTTGT	3042
1498	СССАСАТСТС	AGCATTCTAG	СССТСТТТСА	CTCACTCACC	САССАТАТСА	አ አ ርጥአ ርጥርጥጥ	3102
1499	CCCAGAICIG	AGCATICIAG	GCCIGITICA	CICACICACC	CAUCAIAIUA	AACIAGICII	3102
1500	AACTGTTGAG	CCTTTCCTTT	CATATCCACA	GAAGACACTG	TCTCAAATGT	TGTACCCTTG	3162
1501							
1502	CCATTTAGGA	CTGAACTTTC	CTTAGCCCAA	GGGACCCAGT	GACAGTTGTC	TTCCGTTTGT	3222
1503							
1504	CAGATGATCA	GTCTCTACTG	ATTATCTTGC	TGCTTAAAGG	CCTGCTCACC	AATCTTTCTT	3282
1505							
1506	TCACACCGTG	TGGTCCGTGT	TACTGGTATA	CCCAGTATGT	TCTCACTGAA	GACATGGACT	3342
1507							
1508	TTATATGTTC	AAGTGCAGGA	ATTGGAAAGT	TGGACTTGTT	TTCTATGATC	CAAAACAGCC	3402
1509							
1510	CTATAAGAAG	GTTGGAAAAG	GAGGAACTAT	ATAGCAGCCT	TTGCTATTTT	CTGCTACCAT	3462
1511							
1512	TTCTTTTCCT	CTGAAGCGGC	CATGACATTC	CCTTTGGCAA	CTAACGTAGA	AACTCAACAG	3522
1513 1514	3 3 C 3 MM MM C C	TTTCCTAGAG	man acmmmn	CAMCAMAAMC	C2 C2 2 CM2 M2	CACIONACIONA	3582
1514	AACATTTICC	TITCCIAGAG	ICACCITITA	GAIGAIAAIG	GACAACTATA	GACTIGCTCA	3502
1516	ተተ ርተተር ነር ነር	TGATTGCCCC	тсасстаат	ССУСТСТСТС	таттсатсст	СТТСССААТТ	3642
1517	TIGITERORE	TOATTOCCCC	TEACCIONNI	CCACICICIO	TATTCATOCT	CIIGCAAII	3042
1518	TCTTTGACTT	TCTTTTAAGG	GCAGAAGCAT	TTTAGTTAAT	TGTAGATAAA	GAATAGTTTT	3702
1519							
1520	CTTCCTCTTC	TCCTTGGGCC	AGTTAATAAT	TGGTCCATGG	CTACACTGCA	ACTTCCGTCC	3762
1521							
1522	AGTGCTGTGA	TGCCCATGAC	ACCTGCAAAA	TAAGTTCTGC	CTGGGCATTT	TGTAGATATT	3822
1523							
1524	AACAGGTGAA	TTCCCGACTC	${\tt TTTTGGTTTG}$	AATGACAGTT	CTCATTCCTT	CTATGGCTGC	3882
1525							
1526	AAGTATGCAT	CAGTGCTTCC	CACTTACCTG	ATTTGTCTGT	CGGTGGCCCC	ATATGGAAAC	3942
1527	GGT 4 G 5 T 5 T	mamma = = = = =	7 m 7 cm		man amaaaa =	GG111 ======	4000
1528	CCTGCGTGTC	TGTTGGCATA	ATAGTTTACA	AATGGTTTTT	TCAGTCCTAT	CCAAATTTAT	4002
1529	TCAACCAACA	7 7 7 7 TT 7 7 TT TT 7		G7 G7 T7 7 GG7		CTTC ATTCTC	4000
1530	IGAACCAACA	AAAATAATTA	CITCIGCCCT	GAGATAAGCA	GATTAAGTTT	GITCATTCTC	4062

RAW SEQUENCE LISTING PATENT APPLICATION US/08/083,590

DATE: 12/16/93 TIME: 13:10:55

1532 TGCTTTATTC TCTCCATGTG GCAACATTCT GTCAGCCTCT TTCATAGTGT GCAAACATTT 1121 1533	1 5 2 1																		
1533 1534 1535 1536 1536 1537 1538 26CATTCTCA AATGGTGACT CTCTGCCCTT GGACCCATTT ATTATTCACA GATGGGGAGA 4182 1537 1538 1539 1540 1541 (2) INFORMATION FOR SEQ ID NO:13: 1542 (3) SEQUENCE CHARACTERISTICS: (4) LENGTH: 657 amino acids (B) TYPE: amino acid (C) TOPOLOGY: unknown 1547 1548 (ii) MOLECULE TYPE: protein 1549 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13: 1551 1552 Glu Val Asp Val Leu Asp Val Asn Val Arg Gly Pro Asp Gly Cys Thr 1	1531 1532	ጥረረጥጥ	ידעדי	יידרי יו	יכיייכי	י א ידיכי	דמ מנ	ግ አ አ ር ፖ	י חיויים	ቦ ሬጥ	ግልሮር	יייט	יייירי:	מ יים מיים	ייביי נ	3CN N :	א כי א יחייחיי	1	4122
1536 1536 1537 1538 1539 1540 1541 (2) INFORMATION FOR SEQ ID NO:13: 1542 1543 (3) LENGTH: 657 amino acids (B) TYPE: amino acid (B) TYPE: amino acid (B) TYPE: protein 1549 1550 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13: 1551 1552 Glu Val Asp Val Leu Asp Val Asn Val Arg Gly Pro Asp Gly Cys Thr 1553 1554 1555 Pro Leu Met Leu Ala Ser Leu Arg Gly Gly Ser Ser Asp Leu Ser Asp 1556 1557 1558 Glu Asp Glu Asp Ala Glu Asp Ser Ser Ala Asn Ile Ile Thr Asp Leu 1559 1560 Val Tyr Gln Gly Ala Ser Leu Gln Ala Gln Thr Asp Arg Thr Gly Glu 1561 1561 1564 Met Ala Leu His Leu Ala Ala Arg Tyr Ser Arg Ala Asp Ala Ala Lys 1566 1567 Arg Leu Leu Asp Ala Gly Ala Sp Ala Asn Ala Gln Asp Asn Met Gly 1568 1569 Arg Cys Pro Leu His Ala Ala Val Ala Ala Asp Ala Gln Gly Val Phe 1571 1572 1573 Gln Ile Leu Ile Arg Asn Arg Val Thr Asp Leu Asp Ala Arg Met Asn 115 1576 1577 1578 1578 1579 Met Val Ala Glu Leu Ile Asn Cys Gln Ala Asp Val Asn Ala Val Asp 1579 1570 1571 1572 1573 1574 1575 1576 Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Ala Dlu Gly 1577 1578 Met Val Ala Glu Leu Ile Arg Cys Gln Ala Asp Val Asn Ala Val Asp 1579 1579 1570 1571 1572 1574 1575 1576 Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Ala Val Asp 1579 1570 1571 1572 1573 1574 1575 1576 Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Ala Val Asp 1579 1570 1571 1572 1573 1574 1575 1576 Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Ala Val Asp 1579 1570 1571 1572 1573 1574 1575 1576 Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Ala Val Asp 1579 1570 1571 1572 1573 1574 1575 1576 Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Ala Val Asp 1577 1578 1579 1570 1571 1572 1574 1575 1576 1577 1578 1579 1570 1570 1571 1571 1572 1574 1575 1576 1577 1577 1578 1578 1579 1570 1571 1571 1572 1574 1575 1576 1577 1577 1578 1578 1579 1570 1571 1571 1572 1574 1575 1576 1577 1577 1578 1578 1579 1579 1570 1570 1570 1570 1570 1570 1570 1570		10011	. 1711	10 1		JAI U.	10 00	JAACI	1110.	. 010	CAGC	_1 _ 1	1101	TIAG.	IGI (JCAA	ACAIII		7122
1536 1536 1537 1538 1539 1540 1541 1551		TATCA	ATTC	TA A	AATGO	TGA	CT C	rctg	CCCT	r gg/	ACCC	TTTA	ATT	ATTC	ACA (SATG	GGAGA		4182
ACCTATCTGC ATGGACCCTC ACCATCCTCT GTGCAGCACA CACAGTGCAG GGAGCCAGTG 4242 1537 1538 1539 1540 1541 1541 (2) INFORMATION FOR SEQ ID NO:13: 1542 1543 (3) SEQUENCE CHARACTERISTICS: (4) LENGTH: 657 amino acids (B) TYPE: amino acids (B) TYPE: amino acids (C) TOPOLOGY: unknown 1547 1548 (3) SEQUENCE DESCRIPTION: SEQ ID NO:13: 1551 1552 Glu Val Asp Val Leu Asp Val Asn Val Arg Gly Pro Asp Gly Cys Thr 1																			1102
1538 SCGATGGCGA TGACTTTCTT CCCCTG 4268 1539 1540 (2) INFORMATION FOR SEQ ID NO:13: 1541 (2) INFORMATION FOR SEQ ID NO:13: 1542 (3) SEQUENCE CHARACTERISTICS: (A) LENGTH: 657 amino acids (B) TYPE: amino acid (B) TYPE: amino acid (B) TYPE: amino acid (B) TYPE: protein (A) SEQUENCE DESCRIPTION: SEQ ID NO:13: 1551 (A) LEU Asp Val Asn Val Arg Gly Pro Asp Gly Cys Thr 1553 (A) Leu Asp Val Asn Val Arg Gly Pro Asp Gly Cys Thr 1553 (A) Leu Asp Val Asn Val Arg Gly Pro Asp Gly Cys Thr 1553 (A) Asp Glu Asp Ala Glu Asp Ser Ser Ala Asn Ile Ile Thr Asp Leu Ser Asp 1559 (A) Asp Glu Asp Ala Glu Asp Ser Ser Ala Asn Ile Ile Thr Asp Leu 35 (A) Asp Glu Asp Ala Glu Asp Ser Ser Ala Asn Ile Ile Thr Asp Leu 35 (A) Asp Glu Asp Ala Glu Asp Ser Ser Ala Asn Ile Ile Thr Asp Leu 35 (A) Asp Glu Asp Ala Glu Asp Ala Glu Thr Asp Arg Thr Gly Glu 50 (A) Asp Glu Asp Ala Glu Asp Ala Ala Glu Thr Asp Arg Thr Gly Glu 50 (A) Arg Leu Leu Asp Ala Gly Ala Asp Ala Asn Ala Gln Asp Asn Met Gly 50 (A) Arg Leu Leu Asp Ala Gly Ala Asp Ala Asn Ala Gln Gly Val Phe 1571 (A) Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg Leu Asp Ala Arg Met Asn 115 (A) Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg Leu Ala Arg Leu Ala Arg Met Asn 115 (A) Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Glu Gly 145 (A) Asp Gly Val Ala Glu Leu Ile Asn Cys Gln Ala Asp Val Asn Ala Val Ala Val Asp 145 (A) Asp Gly Val Asn Ala Val Asp Ile (A) Asp Ile Val Ala Glu Gly Ile Val Ala Glu Glu Gly Ile Val Ala Glu Glu Gly Ile Val Val Ala Cys Gln Ala Asp Val Asn Ala Val Asp Ile Val Asp Ile Val Ala Glu Glu Gly Ile Val Ala Glu Glu Gly Ile Val Ala Glu Glu Gly Ile Val Val Ala Glu Glu Gly Ile Val Val Ala Glu Glu Gly Ile Val Val Ala Glu Glu Glu Gly Ile Val Val Ala Glu		ACCTA	TCT	GC A	ATGG	ACCC.	rc A	CAT	CCTC	r GT	GCAG	CACA	CAC	AGTG	CAG (GAG	CCAGTG	}	4242
1539 1540 1541 (2) INFORMATION FOR SEQ ID NO:13: 1542 1543 (i) SEQUENCE CHARACTERISTICS: 1544 (a) LENGTH: 657 amino acids 1545 (B) TYPE: amino acid 1546 (D) TOPOLOGY: unknown 1547 1548 (ii) MOLECULE TYPE: protein 1549 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13: 1550 (Su Val Asp Val Leu Asp Val Asn Val Arg Gly Pro Asp Gly Cys Thr 1551 1552 (Glu Val Asp Val Leu Asp Val Asn Val Arg Gly Pro Asp Gly Cys Thr 1553 1554 1 5 10 15 1555 1554 1 10 15 1555 1555 1 10 15 1556 1 10 15 1557 1 10 15 1558 1 10 15 1559 30 25 30 1557 1 10 15 1558 1 10 10 15 1559 30 45 1559 30 45 1550 1560 1561 Val Tyr Gln Gly Ala Ser Leu Gln Ala Gln Thr Asp Arg Thr Gly Glu 1561 1562 1563 1564 166 166 166 166 166 166 166 166 166 1																			
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1567 Arg Leu Leu Asp Ala Gly Ala Asp Ala Asn Ala Gln Asp Asn Met Gly 1568		•					, •					, ,							
1568		Ara L	eu	Leu	Asp	Ala	Glv	Ala	Asp	Ala	Asn	Ala	Gln	Asp	Asn	Met	Glv		
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1570 Arg Cys Pro Leu His Ala Ala Val Ala Asp Ala Gln Gly Val Phe 1571																			
1571		Arg C	'ys	Pro	Leu	His	Ala	Ala	Val	Ala	Ala	Asp	Ala	Gln	Gly	Val	Phe		
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1574																			
1574	1573	Gln I	le	Leu	Ile	Arg	Asn	Arg	Val	Thr	Asp	Leu	Asp	Ala	Arg	Met	Asn		
1576 Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Glu Gly 1577 130 135 140 1578 1579 Met Val Ala Glu Leu Ile Asn Cys Gln Ala Asp Val Asn Ala Val Asp 1580 145 150 155 160	1574					_					-		-		_				
1577 130 135 140 1578 1579 Met Val Ala Glu Leu Ile Asn Cys Gln Ala Asp Val Asn Ala Val Asp 1580 145 150 155 160																			
1578 1579 Met Val Ala Glu Leu Ile Asn Cys Gln Ala Asp Val Asn Ala Val Asp 1580 145 150 155 160		Asp G	ly	Thr	Thr	${\tt Pro}$	Leu	Ile	Leu	Ala	Ala	Arg	Leu	Ala	Val	Glu	Gly		
1579 Met Val Ala Glu Leu Ile Asn Cys Gln Ala Asp Val Asn Ala Val Asp 1580 145 150 155 160		1	.30					135					140						
1580 145 150 155 160							_												
			7al	Ala	Glu	Leu		Asn	Cys	Gln	Ala	_	Val	Asn	Ala	Val	_		
1581		145					150					155					160		
	1581																		

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1582 1583 1584	Asp	His	Gly	Lys	Ser 165	Ala	Leu	His	Trp	Ala 170	Ala	Ala	Val	Asn	Asn 175	Val
1585 1586 1587	Glu	Ala	Thr	Leu 180	Leu	Leu	Leu	Lys	Asn 185	Gly	Ala	Asn	Arg	Asp 190	Met	Gln
1588 1589 1590	Asp	Asn	Lys 195	Glu	Glu	Thr	Pro	Leu 200	Phe	Leu	Ala	Ala	Arg 205	Glu	Gly	Ser
1591 1592 1593	Tyr	Glu 210	Ala	Ala	Lys	Ile	Leu 215	Leu	Asp	His	Phe	Ala 220	Asn	Arg	Asp	Ile
1594 1595 1596	Thr 225	Asp	His	Met	Asp	Arg 230	Leu	Pro	Arg	Asp	Val 235	Ala	Arg	Asp	Arg	Met 240
1597 1598 1599		His	_		245				_	250	-				255	
1600 1601 1602		Pro	_	260					265					270	_	-
1603 1604 1605		Asn	275					280	_				285	_	_	-
1606 1607 1608		Arg 290					295					300				
1609 1610 1611	305	Ala	_			310			_		315					320
1612 1613 1614		Ser		_	325					330					335	
1615 1616 1617		Asp		340					345					350		
1618 1619 1620 1621		Pro	355					360					365			
1622 1623 1624		370 Ser					375					380				
1625 1626 1627	385	Thr				390					395				-	400
1628 1629 1630		Ser			405					410					415	
1631 1632	val	Set	FIU	420	Set	GTÀ	Set	AIA	425	Ser	пеп	Set	чтА	430	nis	FIO

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1633 1634 1635	Val	Pro	Val 435	Pro	Ala	Asp	Trp	Met 440	Asn	Arg	Met	Glu	Val 445	Asn	Glu	Thr
1636 1637 1638	Gln	Tyr 450	Asn	Glu	Met	Phe	Gly 455	Met	Val	Leu	Ala	Pro 460	Ala	Glu	Ġĺy	Thr
1639 1640 1641	His 465	Pro	Gly	Ile	Ala	Pro 470	Gln	Ser	Arg	Pro	Pro 475	Glu	Gly	Lys	His	Ile 480
1642 1643 1644	Thr	Thr	Pro	Arg	Glu 485	Pro	Leu	Pro	Pro	Ile 490	Val	Thr	Phe	Gln	Leu 495	Ile
1645 1646 1647	Pro	Lys	Gly	Ser 500	Ile	Ala	Gln	Pro	Ala 505	Gly	Ala	Pro	Gln	Pro 510	Gln	Ser
1648 1649 1650	Thr	Cys	Pro 515	Pro	Ala	Val	Ala	Gly 520	Pro	Leu	Pro	Thr	Met 525	Tyr	Gln	Ile
1651 1652 1653	Pro	Glu 530	Met	Ala	Arg	Leu	Pro 535	Ser	Val	Ala	Phe	Pro 540	Thr	Ala	Met	Met
1654 1655 1656	Pro 545	Gln	Gln	Asp	Gly	Gln 550	Val	Ala	Gln	Thr	Ile 555	Leu	Pro	Ala	Tyr	His 560
1657 1658 1659	Pro	Phe	Pro	Ala	Ser 565	Val	Gly	Lys	Tyr	Pro 570	Thr	Pro	Pro	Ser	Gln 575	His
1660 1661 1662	Ser	Tyr	Ala	Ser 580	Ser	Asn	Ala	Ala	Glu 585	Arg	Thr	Pro	Ser	His 590	Ser	Gly
1663 1664 1665	His	Leu	Gln 595	Gly	Glu	His	Pro	Tyr 600	Leu	Thr	Pro	Ser	Pro 605	Glu	Ser	Pro
1666 1667 1668	Asp	Gln 610	Trp	Ser	Ser	Ser	Ser 615	Pro	His	Ser	Ala	Ser 620	Asp	Trp	Ser	Asp
1669 1670 1671	Val 625	Thr	Thr	Ser	Pro	Thr 630	Pro	Gly	Gly	Ala	Gly 635	Gly	Gly	Gln	Arg	Gly 640
1672 1673 1674	Pro	Gly	Thr	His	Met 645	Ser	Glu	Pro	Pro	His 650		Asn		Gln	Val 655	Tyr
1675 1676 1677	Ala															
1678 1679 1680	(2)				FOR											
1681 1682 1683			· (1	A) LI 3) TY	ENGTI (PE : [RANI	H: 77 amir	7 ami	ino a	acids	3						

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1684			(D)	TOI	POLO	3Υ: ι	ınkno	own									
1685																	
1686		(ii)	MOLI	ECULI	E TYI	PE: 1	pept:	ide									
1687																	
1688																	
1689																	
1690		(xi)	SEQ	JENCI	E DES	SCRI	PTIO	N: SI	EQ II	D. NO	:14:						
1691			_		_						_						
1692			Asp	Ile	Asp		Cys	Asp	Gln	Gly		Pro	Cys	Glu	His		Gly
1693		1				5					10					15	
1694					_	_,	_		_	_	_	_	_		_		
1695		Ile	Cys	Val		Thr	Pro	GLY	Ser		Arg	Cys	Asn	Cys		GIn	Gly
1696					20					25					30		
1697			_	_				_			_		_		_		
1698		Phe	Thr	Gly	Pro	Arg	Cys	Glu	Thr	Asn	Ile	Asn	Glu	Cys	Glu	Ser	His
1699				35					40					45			
1700																	
1701		Pro	Cys	Gln	Asn	Glu	Gly	Ser	Cys	Leu	Asp	Asp	Pro	Gly	Thr	Phe	Arg
1702			50					55					60				
1703																	
1704		Cys	Val	Cys	Met	Pro	Gly	Phe	Thr	Gly	Thr	Gln	Cys	Glu			
1705		65					70					75					
1706																	
1707	(2)	INFO	RMAT	ION I	FOR S	SEQ :	ID N	0:15	:								
1708																	
1709		(i)	SEQU	JENCI	E CHA	ARAC:	reri:	STICS	S :								
1709 1710		(i)			E CHA												
1710 1711		(i)	(A)	LEI		: 78	amiı	no a									
1710		(i)	(A)	LEI TYI	NGTH	: 78 amino	amin ac:	no ao id	cids								
1710 1711		(i)	(A) (B) (C)	LEI TYI	NGTH PE: 8	: 78 amino EDNES	amin cac: SS: s	no ad id singl	cids								
1710 1711 1712		(i)	(A) (B) (C)	LEI TYI	NGTH PE: 8 RANDI	: 78 amino EDNES	amin cac: SS: s	no ad id singl	cids								
1710 1711 1712 1713		(i) (ii)	(A) (B) (C) (D)	LEI TYI STI	NGTH PE: & RANDI POLO	: 78 amino EDNES GY: 1	amin o ac: SS: s unkno	no ao id singl own	cids								
1710 1711 1712 1713 1714			(A) (B) (C) (D)	LEI TYI STI	NGTH PE: & RANDI POLO	: 78 amino EDNES GY: 1	amin o ac: SS: s unkno	no ao id singl own	cids								
1710 1711 1712 1713 1714 1715			(A) (B) (C) (D)	LEI TYI STI	NGTH PE: & RANDI POLO	: 78 amino EDNES GY: 1	amin o ac: SS: s unkno	no ao id singl own	cids								
1710 1711 1712 1713 1714 1715 1716			(A) (B) (C) (D)	LEI TYI STI	NGTH PE: & RANDI POLO	: 78 amino EDNES GY: 1	amin o ac: SS: s unkno	no ao id singl own	cids								
1710 1711 1712 1713 1714 1715 1716 1717			(A) (B) (C) (D)) LEI) TYI) STI) TOI	NGTH PE: 6 RANDI POLOG	: 78 amino EDNES GY: 1	amino ac: SS: sunkno pept:	no ad id sing: own ide	cids le	ои с	: 15 :						
1710 1711 1712 1713 1714 1715 1716 1717 1718		(ii) (xi)	(A) (B) (C) (D) MOLI) LEI) TYI) STI) TOI ECULI	NGTH PE: 6 RANDI POLOG E TYI E DES	: 78 amino EDNES GY: 1 PE: 1	amino ac: SS: sunkno pept:	no adid sing own ide N: SI	cids le EQ II								
1710 1711 1712 1713 1714 1715 1716 1717 1718 1719		(ii) (xi)	(A) (B) (C) (D) MOLI) LEI) TYI) STI) TOI ECULI	NGTH PE: 6 RANDI POLOG E TYI E DES	: 78 amino EDNES GY: 1 PE: 1	amino ac: SS: sunkno pept:	no adid sing own ide N: SI	cids le EQ II			Asn	Pro	Cys	Glu	His	Gly
1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720		(ii) (xi)	(A) (B) (C) (D) MOLI) LEI) TYI) STI) TOI ECULI	NGTH PE: 6 RANDI POLOG E TYI E DES	: 78 amino EDNES GY: 1 PE: 1	amino ac: SS: sunkno pept:	no adid sing own ide N: SI	cids le EQ II			Asn	Pro	Cys	Glu	His 15	Gly
1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723		(ii) (xi) Asn	(A) (B) (C) (D) MOLH) LEI) TYI) STI) TOI ECULI UENCI	NGTH PE: { RANDI POLOG E TYI E DES Asp	: 78 amino EDNES GY: 1 PE: 1 GCRII Glu 5	amino ac: SS: sunkno pept: PTION	no ad id singi own ide N: SI	cids le EQ II Leu	Gly	Ala 10					15	
1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722		(ii) (xi) Asn	(A) (B) (C) (D) MOLI) LEI) TYI) STI) TOI ECULI UENCI	NGTH PE: { RANDI POLOG E TYI E DES Asp	: 78 amino EDNES GY: 1 PE: 1 GCRII Glu 5	amino ac: SS: sunkno pept: PTION	no ad id singi own ide N: SI	cids le EQ II Leu	Gly Ser	Ala 10					15	
1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723		(ii) (xi) Asn	(A) (B) (C) (D) MOLH) LEI) TYI) STI) TOI ECULI UENCI	NGTH PE: { RANDI POLOG E TYI E DES Asp	: 78 amino EDNES GY: 1 PE: 1 GCRII Glu 5	amino ac: SS: sunkno pept: PTION	no ad id singi own ide N: SI	cids le EQ II Leu	Gly	Ala 10					15	
1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724		(ii) (xi) Asn	(A) (B) (C) (D) MOLH) LEI) TYI) STI) TOI ECULI UENCI	NGTH PE: & RANDI POLOG E TYI E DES Asp	: 78 amino EDNES GY: 1 PE: 1 GCRII Glu 5	amino ac: SS: sunkno pept: PTION	no ad id singi own ide N: SI	cids le EQ II Leu	Gly Ser	Ala 10				Cys	15	
1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725		(ii) (xi) Asn 1	(A) (B) (C) (D) MOLH) LEI) TYI) STI) TOI ECULI UENCI Val	NGTH PE: & RANDI POLOG E TYI E DES Asp Thr 20	: 78 amind EDNES GY: 1 PE: p GCRII Glu 5 Asn	amino ac: SS: sunknow pept: PTION Cys	no ad id sings own ide N: SI Ser	cids le EQ II Leu Gly	Gly Ser 25	Ala 10 Phe	Gln	Cys	Asn	Cys 30	15 Pro	Gln
1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725 1726		(ii) (xi) Asn 1	(A) (B) (C) (D) MOLH SEQUASP) LEI) TYI) STI) TOI ECULI UENCI Val	NGTH PE: & RANDI POLOG E TYI E DES Asp Thr 20	: 78 amind EDNES GY: 1 PE: p GCRII Glu 5 Asn	amino ac: SS: sunknow pept: PTION Cys	no ad id sings own ide N: SI Ser	cids le EQ II Leu Gly	Gly Ser 25	Ala 10 Phe	Gln	Cys	Asn	Cys 30	15 Pro	Gln
1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725 1726 1727 1728 1729		(ii) (xi) Asn 1	(A) (B) (C) (D) MOLH SEQUASP) LET) TYI) STI) TOI ECULI VAL Cys Ala	NGTH PE: & RANDI POLOG E TYI E DES Asp Thr 20	: 78 amind EDNES GY: 1 PE: p GCRII Glu 5 Asn	amino ac: SS: sunknow pept: PTION Cys	no ad id sings own ide N: SI Ser	cids le EQ II Leu Gly Glu	Gly Ser 25	Ala 10 Phe	Gln	Cys	Asn Glu	Cys 30	15 Pro	Gln
1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725 1726 1727		(ii) (xi) Asn 1 Gly	(A) (B) (C) (D) MOLH SEQUASP) LEI) TYI) STI) TOI ECULI UENCI Val Cys Ala 35	MGTH PE: ARANDI POLOG E TYI E DES Asp Thr 20 Gly	: 78 amind EDNES GY: 1 PE: p SCRII Glu 5 Asn Pro	amino ac: SS: SS: SINKNO PETION Cys Thr	no adid sings own ide N: SI Ser Leu Cys	cids le EQ II Leu Gly Glu 40	Gly Ser 25 Ile	Ala 10 Phe Asp	Gln Val	Cys Asn	Asn Glu 45	Cys 30	15 Pro Leu	Gln Ser
1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725 1726 1727 1728 1729		(ii) (xi) Asn 1 Gly	(A) (B) (C) (D) MOLH SEQU Asp) LEI) TYI) STI) TOI ECULI UENCI Val Cys Ala 35	MGTH PE: ARANDI POLOG E TYI E DES Asp Thr 20 Gly	: 78 amind EDNES GY: 1 PE: p SCRII Glu 5 Asn Pro	amino ac: SS: SS: SINKNO PETION Cys Thr	no adid sings own ide N: SI Ser Leu Cys	cids le EQ II Leu Gly Glu 40	Gly Ser 25 Ile	Ala 10 Phe Asp	Gln Val	Cys Asn	Asn Glu 45	Cys 30	15 Pro Leu	Gln Ser
1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725 1726 1727 1728 1729 1730		(ii) (xi) Asn 1 Gly Gly Asn	(A) (B) (C) (D) MOLI SEQUARY Arg Tyr) LET) TYI) STI) TOI ECULI UENCI Val Cys Ala 35	NGTH PE: { RANDI POLOG E TYI E DES Asp Thr 20 Gly Gln	: 78 amind EDNES GY: 1 PE: 1 CCRII Glu 5 Asn Pro Asn	amino ac: SS: sunknow pept: PTION Cys Thr Arg Asp	no adid sing own ide N: SI Ser Leu Cys Ser 55	cids le EQ II Leu Gly Glu 40 Thr	Gly Ser 25 Ile Cys	Ala 10 Phe Asp	Gln Val Asp	Cys Asn Gln 60	Asn Glu 45 Ile	Cys 30 Cys Gly	15 Pro Leu	Gln Ser
1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725 1726 1727 1728 1729 1730 1731		(ii) (xi) Asn 1 Gly Gly Asn	(A) (B) (C) (D) MOLI SEQUARY Arg Tyr) LET) TYI) STI) TOI ECULI UENCI Val Cys Ala 35	NGTH PE: { RANDI POLOG E TYI E DES Asp Thr 20 Gly Gln	: 78 amind EDNES GY: 1 PE: 1 CCRII Glu 5 Asn Pro Asn	amino ac: SS: sunknow pept: PTION Cys Thr Arg Asp	no adid sing own ide N: SI Ser Leu Cys Ser 55	cids le EQ II Leu Gly Glu 40 Thr	Gly Ser 25 Ile Cys	Ala 10 Phe Asp	Gln Val Asp	Cys Asn Gln 60	Asn Glu 45 Ile	Cys 30 Cys Gly	15 Pro Leu	Gln Ser
1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725 1726 1727 1728 1729 1730 1731 1732		(ii) (xi) Asn 1 Gly Gly Asn	(A) (B) (C) (D) MOLI SEQUARY Arg Tyr) LET) TYI) STI) TOI ECULI UENCI Val Cys Ala 35	NGTH PE: { RANDI POLOG E TYI E DES Asp Thr 20 Gly Gln	: 78 amind EDNES GY: 1 PE: 1 CCRII Glu 5 Asn Pro Asn	amino ac: SS: sunknow pept: PTION Cys Thr Arg Asp	no adid sing own ide N: SI Ser Leu Cys Ser 55	cids le EQ II Leu Gly Glu 40 Thr	Gly Ser 25 Ile Cys	Ala 10 Phe Asp	Gln Val Asp	Cys Asn Gln 60	Asn Glu 45 Ile	Cys 30 Cys Gly	15 Pro Leu	Gln Ser

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1735																	
1736																	
1737	(2)	INFO	RMAT:	ION I	FOR S	SEQ :	ID N	0:16	:								
1738																	
1739		(i)	SEQ	UENC	E CH	ARAC'	TERI:	STIC	S :								
1740			(A)) LEI	NGTH	: 65	4 am	ino a	acida	5							
1741			(B	TY	PE: a	amino	o ac	id									
1742			(C		RANDI			_	le								
1743			(D) TO	POLO	3Y: 1	unkno	own									
1744					_												
1745		(ii)	MOL:	ECULI	E TY	PE:]	pept:	ıde									
1746																	
1747																	
1748																	
1749 1750		(xi)	CEO	TENTO	- De	CD T	וחדיים	л. С1	- TI) NO	.16.						
1751		(XI)	SEQ	JENCI	e De:	SCRI.	PIIO	N: D1	נד אַנ	טאו כ	:10:						
1752		Thr	Dro	Dro	Gln	Gl v	Glu	Tl۵	Glu	Δla	Agn	Cve	Mot	Aen	Va l	Asn	Va 1
1753		1	110	110	GIII	5	Giu	110	GIU	AIG	10	Суз	Mec	vah	vai	15	val
1754		-				•					-0					13	
1755		Ara	Glv	Pro	Asp	Glv	Phe	Thr	Pro	Leu	Met	Tle	Δla	Ser	Cvs	Ser	Glv
1756		5	U -1		20	0-1				25				-	30	-	- 1
1757																	
1758		Gly	Gly	Leu	Glu	Thr	Gly	Asn	Ser	Glu	Glu	Glu	Glu	Asp	Ala	Ser	Ala
1759		-	•	35			_		40					45			
1760																	
1761		Asn	Met	Ile	Ser	Asp	Phe	Ile	Gly	Gln	Gly	Ala	Gln	Leu	His	Asn	Gln
1762			50					55					60				
1763																	
1764		Thr	Asp	Arg	Thr	Gly	Glu	Thr	Ala	Leu	His	Leu	Ala	Ala	Arg	Tyr	Ala
1765		65					70					75					80
1766														_		_	
1767		Arg	Ala	Asp	Ala		Lys	Arg	Leu	Leu		Ser	Ser	Ala	Asp	Ala	Asn
1768						85					90					95	
1769		7707	<i>0</i> 15	7. ~~	7	Mot	<u>ما</u>	7. ~~~	mb	Dwo	T 0.11	TT i o	7.7.	77.	1707	777.	77.
1770 1771		vai	GIII	Asp	100	Mec	GIY	Arg	IIII	105	Lеu	птв	АТА	Ala		Ala	Ата
1772					100					105					110		
1773		Agn	Δla	Gln	Glv	Va 1	Phe	Gln	Tle	T.e.11	Tle	Ara	Δsn	Ara	Δla	Thr	Agn
1774		nop	mu	115	CLY	•41	1110	0111	120	LCu		11119	71011	125	mu		TIDE
1775																	
1776		Leu	Asp	Ala	Arq	Met	Phe	Asp	Gly	Thr	Thr	Pro	Leu	Ile	Leu	Ala	Ala
1777			130					135	-				140				
1778																	
1779		Arg	Leu	Ala	Val	Glu	Gly	Met	Val	Glu	Glu	Leu	Ile	Asn	Ala	His	Ala
1780		145					150					155					160
1781																	
1782		Asp	Val	Asn	Ala		Asp	Glu	Phe	Gly	_	Ser	Ala	Leu	His	\mathtt{Trp}	Ala
1783						165					170					175	
1784		7A T .	7.7 -	77 7	7	7	17 T	7	70 T -	7 .7.	7 7 -	17- 7	T	T	T	70	0
1785		ата	ата	vaı	Asn	Asn	vaı	Asp	ата	АТА	ата	vaı	ьeu	ьeu	ьys	Asn	ser

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1786				180					185					190		
1787						~1		_	_	~ 1	~1	1		_	-,	_
1788	Ата	ASII	_	Asp	мет	GIN	ASII		ьys	GIU	GIU	Thr	Ser	Leu	Pne	Leu
1789			195					200					205			
1790 1791	חות	חות	7. ~~~	C1.,	C1.,	C 0 20	Птт	a1.,	mb se	חות	Tura	1701	T	т	7) (7)	TT i a
1792	MIA	210	Arg	GIU	GIY	ser	_	GIU	IIII	ALA	пур		Leu	ьeu	Asp	пір
1793		210					215					220				
1794	Та гъс	71-	7 an	7. **	7 ~~	Tla	The	7 ~~	TI i a	Mot	7	7 200	Leu	Dago	7. 200	70.00
1795	225	Ата	ASII	Arg	Asp	230	1111	Asp	птв	Mec	235	Arg	ьeu	PIO	Arg	
1796	225					230					233					240
1797	тіо	71-	Cln	C1,,	λνα	Mot	шic	ui c	7 cm	Tla	17a l	шia	T 011	T 011	7 00	Clu
1798	116	нта	GIII	GIU	245	MEC	nis	птъ	Asp	250	vaı	птъ	Leu	пец	255	GIU
1799					243					250					233	
1800	Туг	Δen	T.011	V-1	Lvc	Sar	Dro	Thr	T.A11	Hic	Δen	Glv	Pro	T. - 211	Gl v	בות
1801	TYL	ASII	DC u	260	шуз	261	110	1111	265	1115	MOII	GLY	110	270	GLY	Ата
1802				200					205					2/0		
1803	Thr	Thr	T.A11	Ser	Pro	Pro	Tle	Cve	Ser	Dro	Δen	Glv	Tyr	Mot	Glv	Δan
1804	1111	1111	275	JCI	110	110	110	280	DCI	110	ASII	OLY	285	Mec	GLY	ASII
1805			2,3					200					205			
1806	Met.	Lvs	Pro	Ser	Val	Gln	Ser	Lvs	Lvs	Ala	Ara	Lvs	Pro	Ser	Tle	Lvs
1807		290					295	-, 5	_, 5		5	300		501		270
1808												500				
1809	Glv	Asn	Glv	Cvs	Lvs	Glu	Ala	Lvs	Glu	Leu	Lvs	Ala	Arg	Ara	Lvs	Lvs
1810	305		0-1	-1-	-1-	310		-1-			315		5	5	-1-	320
1811	505					3_0										320
1812	Ser	Gln	Asp	Glv	Lvs	Thr	Thr	Leu	Leu	Asp	Ser	Glv	Ser	Ser	Glv	Val
1813				1	325					330		1			335	
1814																
1815	Leu	Ser	Pro	Val	asp	Ser	Leu	Glu	Ser	Thr	His	Glv	Tyr	Leu	Ser	asp
1816				340	-				345			_	-	350		_
1817																
1818	Val	Ser	Ser	Pro	Pro	Leu	Met	Thr	Ser	Pro	Phe	Gln	Gln	Ser	Pro	Ser
1819			355					360					365			
1820																
1821	Met	Pro	Leu	Asn	His	Leu	Thr	Ser	Met	Pro	Glu	Ser	Gln	Leu	Gly	Met
1822		370					375					380				
1823																
1824	Asn	His	Ile	Asn	Met	Ala	Thr	Lys	Gln	Glu	Met	Ala	Ala	Gly	Ser	Asn
1825	385					390					395					400
1826																
1827	Arg	Met	Ala	Phe	Asp	Ala	Met	Val	${\tt Pro}$	Arg	Leu	Thr	His	Leu	Asn	Ala
1828					405					410					415	
1829																
1830	Ser	Ser	Pro	Asn	Thr	Ile	Met	Ser	Asn	Gly	Ser	Met	His		Thr	Val
1831				420					425					430		
1832																
1833	Gly	Gly		Pro	Thr	Met	Asn		Gln	Cys	Asp	${\tt Trp}$	Leu	Ala	Arg	Leu
1834			435					440					445			
1835		_					_		_	_	_		_	_		
1836	Gln	Asn	Gly	Met	Val	Gln	Asn	Gln	Tyr	Asp	Pro	Ile	Arg	Asn	Gly	Ile

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1837			450					455					460				
1838		a1	a1	al. .	70	70.7 -	a1	~1	7.7 -	a 1	70.7 -	.	a1	77.5	a 1	-	
1839			GIII	GIY	ASII	Ата		GIII	Ата	GIN	Ala		GIII	HIS	GIY	Leu	
1840 1841		465					470					475					480
1842		Thr	802	T 011	цiс	7 an	C1	T 011	Dro	חות	The	The	T 011	Com	C1 n	Mob	Mob
1843		1111	ser	ьeu	птѕ	485	GLY	ьеи	PIO	Ата	490	Inr	ьeu	ser	GIII	Met	Met
1844						400					490					495	
1845		Thr	Tur	Gln	Δla	Met	Pro	Δen	Thr	Δνα	T.011	Δla	Δen	Gln	Pro	His	T.011
1846		1111	- y -	GIII	500	Mec	110	MOII	1111	505	пец	ліа	voii	GIII	510	птэ	пец
1847					300					505					310		
1848		Met	Gln	Δla	Gln	Gln	Met	Gln	Gln	Gln	Gln	Δan	T.e.ii	Gln	T.e.u	His	Gln
1849			0	515	0	0		04.11	520	01 11		11011		525	DC W	****	0111
1850				J					320					J 2 J			
1851		Ser	Met	Gln	Gln	Gln	His	His	Asn	Ser	Ser	Thr	Thr	Ser	Thr	His	Tle
1852		201	530		5			535			501		540	501			
1853																	
1854		Asn	Ser	Pro	Phe	Cvs	Ser	Ser	Asp	Ile	Ser	Gln	Thr	Asp	Leu	Gln	Gln
1855		545				•	550					555					560
1856																	
1857		Met	Ser	Ser	Asn	Asn	Ile	His	Ser	Val	Met	Pro	Gln	Asp	Thr	Gln	Ile
1858						565					570			-		575	
1859	•																
1860		Phe	Ala	Ala	Ser	Leu	Pro	Ser	Asn	Leu	Thr	Gln	Ser	Met	Thr	Thr	Ala
1861					580					585					590		
1862																	
1863		Gln	Phe	Leu	Thr	Pro	Pro	Ser	Gln	His	Ser	Tyr	Ser	Ser	${\tt Pro}$	Met	Asp
1864				595					600					605			
1865																	
1866		Asn		Pro	Ser	His	Gln	Leu	Gln	Val	Pro	Asp		Pro	Phe	Leu	Thr
1867			610					615					620				
1868		_	_	_	~ 7	_	_	_	~ 3	_	_	_	_	_	_		_
1869			ser	Pro	GIu	Ser		Asp	GIn	Trp	Ser		Ser	Ser	Pro	His	
1870		625					630					635					640
1871		7. ~~	Mah	0	7	Пиль	C	a1	a1	т1.			Dece	D	ml		
1872		ASII	мес	ser	Asp	-	ser	GIU	GIY	тте		ser	Pro	Pro	inr		
1873 1874						645					650						
1875	(2)	TNEOI	יייי אואכ	TON 1	מסם	י בי	או מ	1.17	_								
1876	(2)	INFO	CIMAI.	LOIN	OK	υ .	ואן עו	J: 1 /	•						,		
1877		(i)	SEQU	TENICI	7 CU	ים א <i>כ</i> ים	ד סיבוי	ביידרי	2.								
1878		(1)) LEI						2							
1879				TY					2014	•							
1880				STI					le								
1881				TOI					_								
1882			7					_									
1883		(ii)	MOLI	ECULI	TYI	PE: 1	ept:	ide									
1884		-				•	-										
1885																	
1886																	
1887		(xi)	SEQ	JENCI	E DES	SCRIE	OITS	V: SI	EQ II	ON C	:17:						

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1888																
1889	Thr	Pro	Pro	Gln	Gly	Glu	Val	Asp	Ala	Asp	Cys	Met	Asp	Val	Asn	Val
1890	1				5			_		10	•		_		15	
1891																
1892	Arg	Gly	Pro	Asp	Gly	Phe	Thr	Pro	Leu	Met	Ile	Ala	Ser	Cys	Ser	Gly
1893	_	-		20	•				25					30		•
1894																
1895	Glv	Gly	Leu	Glu	Thr	Glv	Asn	Ser	Glu	Glu	Glu	Glu	Asp	Ala	Pro	Ala
1896		2	35			1		40					45			
1897																
1898	Val	Ile	Ser	Asp	Phe	Ile	Tvr	Gln	Glv	Ala	Ser	Leu	His	Asn	Gln	Thr
1899		50					55		1			60				
1900																
1901	Asp	Arg	Thr	Glv	Glu	Thr	Δla	Leu	His	Leu	Δla	Ala	Ara	Tvr	Ser	Ara
1902	65	9		0-1		70					75		9	-1-		80
1903	0.0										, ,					•
1904	Ser	Asp	Δla	Δla	Lve	Δrα	T.e.11	Len	Glu	Δla	Ser	Δla	Agn	Δla	Δen	Tle
1905	001	110p	1114	1114	85	9	LCu	пси	O L CL	90	OCI	mu	пор	7114	95	
1906					0.5					20					23	
1907	Gln	Asp	Δsn	Met	Glv	Δrα	Thr	Pro	T.e.11	His	Δla	Δla	Val	Ser	Δla	Agn
1908	0111	ADP	ADII	100	017	nr 9		110	105	1110	ALU	ALU	vai	110	ALU	лор
1909				100					103					110		
1910	Δla	Gln	Glv	Val	Dha	Gln	Tla	T.011	Len	Ara	Λen	Λrα	בות	Thr	λen	T.611
1911	AIA	GIII	115	val	FIIC	GIII	116	120	цец	Arg	MSII	Arg	125	1111	ASP	ьец
1912			113					120					123			
1913	7 cn	Ala	Λrα	Mat	uic	7 en	G137	Thr	Thr	Dro	Leu	Tla	Leu	773	7715	7 ra
1914	Asp	130	Arg	MEC	птэ	ASP	135	TIII	1111	PIO	цец	140	ьeu	Ата	мта	Arg
1915		130					133					140				
	T 011	770	v-1	al. ,	~1··	Mat	T 011	~1	7 ~~	T 011	T1.	7) cr	Com	TT : 0	777	7.00
1916		Ala	vaı	GIU	GIA		ьeu	GIU	Asp	ьeu		ASII	ser	HIS	Ата	_
1917	145					150					155					160
1918	170]	7	77.	7707	7	7	T	a1	T	0	77-	т	TT-2		77-	77-
1919	val	Asn	ALA	vaı	_	Asp	ьeu	GTA	гуѕ		Ата	ьeu	HIS	rrp		Ala
1920					165					170					175	
1921	77.	370]	7. ~~~	7. ~~~	7707	7. ~~	77.	77-	7707	17-1	T	T	T	7	~1	77.
1922	Ald	Val	ASII		Val	Asp	Ата	Ата		val	ьeu	ьeu	гуѕ		GIY	Ala
1923				180					185					190		
1924	7	T	7	M - +	~1 m	7	7	T	a1	a1	mb	Dage	T	Dh.	т	77.
1925	ASII	Lys	_	Met	GIII	ASII	ASII	-	GIU	GIU	IIII	Pro		Pne	ьeu	Ala
1926			195					200					205			
1927	77-	7	a1	a1	00.00	W	a1	mb	77.	T	170]	т	T	7. ~~~	TT	Dha
1928	Ата	Arg	GIU	GTA	ser	Tyr		Inr	ALA	гуѕ	vai		ьeu	Asp	HIS	Pne
1929		210					215					220				
1930	77-	7	7	7	T1 -	mb	7	774 -	N/ - +	7	7	T	D	7	7.0	T1 -
1931		Asn	Arg	ASP	тте		ASP	uis	Mec	ASP		ьeu	Pro	arg	ASD	
1932	225					230					235					240
1933	7.7	<u>م</u> 1	α1	7\	Mo+	114 ~	11 - ~	7.~~	T1 ~	770 T	7	T 011	T 011	7\ ~~	c1	Tree
1934	ATG	Gln	GIU	Arg		nis	HIS	Asp	тте		Arg	ьeu	ьeu	Asp		ryr
1935					245					250					255	
1936	7	T cor	170 T	7)	C	D	<u>ما</u>	T cor	TT - ~	a1	mb	71 -	T 011	a1	C1	Th
1937	ASN	Leu	va⊥	_	ser	Pro	GIII	ьeu		σтУ	ınr	ALA	ьeu	_	стА	Inr
1938				260					265					270		

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1939																
1940	Pro	Thr	Leu	Ser	Pro	Thr	Leu	Cys	Ser	Pro	Asn	Gly	Tyr	Leu	Gly	Asn
1941			275					280				•	285		•	
1942																
1943	Leu	Lys	Ser	Ala	Thr	Gln	Gly	Lys	Lys	Ala	Arg	Lys	Pro	Ser	Thr	Lys
1944		290					295	_	_		_	300				
1945																
1946	Gly	Leu	Ala	Cys	Ser	Ser	Lys	Glu	Ala	Lys	Asp	Leu	Lys	Ala	Arg	Arg
1947	305			_		310					315					320
1948																
1949	Lys	Lys	Ser	Gln	Asp	Gly	Lys	Gly	Cys	Leu	Leu	Asp	Ser	Ser	Ser	Met
1950	-	_			325	_	_	_	_	330		_			335	
1951																
1952	Leu	Ser	Pro	Val	Asp	Ser	Leu	Glu	Ser	Pro	His	Gly	Tyr	Leu	Ser	Asp
1953				340	_				345			_	_	350		_
1954																
1955	Val	Ala	Ser	Pro	Pro	Leu	Pro	Ser	Pro	Phe	Gln	Gln	Ser	Pro	Ser	Met
1956			355					360					365			
1957																
1958	Pro	Leu	Ser	His	Leu	Pro	Gly	Met	Pro	Asp	Thr	His	Leu	Gly	Ile	Ser
1959		370					375			_		380		_		
1960																
1961	His	Leu	Asn	Val	Ala	Ala	Lys	Pro	Glu	Met	Ala	Ala	Leu	Ala	Gly	Gly
1962	385					390					395					400
1963																
1964	Ser	Arg	Leu	Ala	Phe	Glu	Pro	Pro	Pro	Pro	Arg	Leu	Ser	His	Leu	Pro
1965		_			405					410					415	
1966																
1967	Val	Ala	Ser	Ser	Ala	Ser	Thr	Val	Leu	Ser	Thr	Asn	Gly	Thr	Gly	Ala
1968				420					425					430		
1969																
1970	Met	Asn	Phe	Thr	Val	Gly	Ala	Pro	Ala	Ser	Leu	Asn	Gly	Gln	Cys	Glu
1971			435					440					445			
1972																
1973	Trp	Leu	Pro	Arg	Leu	Gln	Asn	Gly	Met	Val	Pro	Ser	Gln	Tyr	Asn	Pro
1974		450					455					460				
1975																
1976	Leu	Arg	Pro	Gly	Val	Thr	Pro	Gly	Thr	Leu	Ser	Thr	Gln	Ala	Ala	
1977	465					470					475					480
1978																
1979	Leu	Gln	His	Gly	Met	Met	Ser	Pro	Ile		Ser	Ser	Leu	Ser		Asn
1980					485					490					495	
1981																_
1982	Thr	Leu	Ser		Ile	Ile	Tyr	Gln	_	Leu	Pro	Asn	Thr	Arg	Leu	Ala
1983				500					505					510		
1984													_		_	_
1985	Thr	Gln		His	Leu	Val	Gln		Gln	Gln	Val	Gln		Gln	Asn	Leu
1986			515					520					525			
1987				_		_	_		_	_	_	~-3	_	•	_	_
1988	Gln		Gln	Pro	GIn	Asn		GIn	Pro	Pro	Ser		Pro	His	Leu	ser
1989		530					535					540				

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1990																	
1991		Val	Ser	Ser	Δla	Δla	Δan	Glv	Hie	T.A11	Glv	Δνα	Sar	Dha	T.A11	Sar	Gly
1992		545	001			1114	550	017	*****	LCu	Cry	555	JCI	1110	пси	DCI	560
1993		313					550					555					500
1994		Glu	Pro	Sar	Gln	Δla	Agn	Val	Gln	Dro	T.011	Glv	Dro	Sar	Sar	LAU	Pro
1995		o_u	110	001	0111	565	пор	vul	0111	110	570	Cry	110	Jer	JCI	575	FIO
1996						303					3,0					3,3	
1997		Val	Hic	Thr	Ile	T.A11	Pro	Gln	Glu	Sar	Gln	בות	Lau	Dro	Thr	Sar	T 011
1998		vai	птэ	1111	580	пец	PIO	GIII	GIU	585	GIII	ніа	пеп	PIO	590	ser	цец
1999					360					202					590		
2000		Dro	Com	Com	Mot	1707	Dwo	Dwo	Mot	mb se	mb se	mb.ss	71 -	Dha	T	mb	D
		PIO	ser		Met	vai	PIO	PIO		1111	1111	1111	GIII		Leu	1111	PIO
2001				595					600					605			
2002				~ 1					~	~	_		_	_	1	_	_
2003		Pro		GIn	His	Ser	Tyr		Ser	Ser	Pro	Val	_	Asn	Thr	Pro	Ser
2004			610					615					620				
2005					_	_		_			_		_				
2006			Gln	Leu	Gln	Val		Glu	His	Pro	Phe	Leu	Thr	Pro	Ser	Pro	Glu
2007		625					630					635					640
2008																	
2009		Ser	Pro	Asp	Gln	Trp	Ser	Ser	Ser	Ser	Arg	His	Ser	Asn	Ile	Ser	Asp
2010						645					650					655	
2011																	
2012		${\tt Trp}$	Ser	Glu	Gly	Ile	Ser	Ser	Pro	Pro	Thr						
2013					660					665							
2014																	
2015																	
2013	(2)	INFO	TAMS:	ION I	FOR S	SEQ :	D NO	18:	:								
2015	(2)	INFO	RMAT	ION 1	FOR S	SEQ :	D NO	0:18	:								
2016	(2)																
2016 2017	(2)	(i)	SEQ	JENCI	E CHA	ARAC:	reris	STICS	S:	3							
2016 2017 2018	(2)		SEQUAL (A)	JENCI	E CHA	ARAC' : 681	reris Lami	STICS ino a	S:	5							
2016 2017 2018 2019	(2)		SEQUAL (A)	JENCI LEI	E CHANGTH:	ARACT	TERIS Lami	STICS ino a	S: acids	3							
2016 2017 2018 2019 2020	(2)		SEQUAL (A)	UENCI LEI TYI	E CHANGTH: PE: &	ARACT 681 amino	TERIS Lami Daci	STICS ino a id singl	S: acids	5							
2016 2017 2018 2019 2020 2021	(2)		SEQUAL (A)	UENCI LEI TYI	E CHANGTH:	ARACT 681 amino	TERIS Lami Daci	STICS ino a id singl	S: acids	3							
2016 2017 2018 2019 2020 2021 2022	(2)	(i)	SEQUAL (A)	UENCI LEI TYI STI	E CHANGTH: PE: 6 RANDE	ARACT : 681 amino EDNES	TERIS L ami c aci SS: s unkno	STICS ino a id singl	S: acids	5							
2016 2017 2018 2019 2020 2021 2022 2023	(2)		SEQUAL (A)	UENCI LEI TYI STI	E CHANGTH: PE: 6 RANDE	ARACT : 681 amino EDNES	TERIS L ami c aci SS: s unkno	STICS ino a id singl	S: acids	3							
2016 2017 2018 2019 2020 2021 2022 2023 2024	(2)	(i)	SEQUAL (A)	UENCI LEI TYI STI	E CHANGTH: PE: 6 RANDE	ARACT : 681 amino EDNES	TERIS L ami c aci SS: s unkno	STICS ino a id singl	S: acids	3							
2016 2017 2018 2019 2020 2021 2022 2023 2024 2025	(2)	(i)	SEQUAL (A)	UENCI LEI TYI STI	E CHANGTH: PE: 6 RANDE	ARACT : 681 amino EDNES	TERIS L ami c aci SS: s unkno	STICS ino a id singl	S: acids	3							
2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026	(2)	(i) (ii)	SEQUENCE (A) (B) (C) (D) MOLI	UENCI) LEI) TYI) STI) TOI	E CHA NGTH: PE: & RANDE POLOC E TYE	ARACT : 683 amino EDNES EY: 1	reris Lami Daci SS: s unkno	STICS ino a id singl own ide	S: acids Le		.19.						
2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027	(2)	(i)	SEQUENCE (A) (B) (C) (D) MOLI	UENCI) LEI) TYI) STI) TOI	E CHA NGTH: PE: & RANDE POLOC E TYE	ARACT : 683 amino EDNES EY: 1	reris Lami Daci SS: s unkno	STICS ino a id singl own ide	S: acids Le		:18:						
2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028	(2)	(ii) (ii)	SEQU (A) (B) (C) (D) MOLI	UENCI TYI TOI ECULI	E CHANGTH: PE: 6 RANDE POLOC E TYI	ARACT : 683 amino EDNES EY: 1	TERIS Lami Daci SS: s unkno Depti	ino a id singl own ide	S: acids Le	ONO:		Circ	Mot	Nan-	vol	ħ a p	Val
2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029	(2)	(ii) (ii) (xi) Thr	SEQU (A) (B) (C) (D) MOLI	UENCI TYI TOI ECULI	E CHA NGTH: PE: & RANDE POLOC E TYE	ARAC: 683 amino EDNES GY: 0 PE: 1	TERIS Lami Daci SS: s unkno Depti	ino a id singl own ide	S: acids Le	ONO:	Asp	Суз	Met	Asp	Val		Val
2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030	(2)	(ii) (ii)	SEQU (A) (B) (C) (D) MOLI	UENCI TYI TOI ECULI	E CHANGTH: PE: 6 RANDE POLOC E TYI	ARACT : 683 amino EDNES EY: 1	TERIS Lami Daci SS: s unkno Depti	ino a id singl own ide	S: acids Le	ONO:		Суз	Met	Asp	Val	Asn 15	Val
2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031	(2)	(ii) (ii) (xi) Thr 1	SEQUENCE SEQUENCE Pro	UENCI) LEI) TYI) STI) TOI ECULI	E CHANGTH: PE: & RANDE POLOG E TYPE E DES	ARACT : 683 amino EDNES EY: 1 PE: 1 GCRII Gly 5	TERIS L ami D aci SS: s unknow Dept:	STICS ino a id singl swn ide Val	S: acids Le EQ II	O NO:	Asp 10	•				15	
2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032	(2)	(ii) (ii) (xi) Thr 1	SEQUENCE SEQUENCE Pro	UENCI) LEI) TYI) STI) TOI ECULI	E CHANGTH: PE: 6 RANDE POLOG E TYPE E DES	ARACT : 683 amino EDNES EY: 1 PE: 1 GCRII Gly 5	TERIS L ami D aci SS: s unknow Dept:	STICS ino a id singl swn ide Val	S: acids Le EQ II	O NO: Ala Leu	Asp 10	•			Cys	15	
2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033	(2)	(ii) (ii) (xi) Thr 1	SEQUENCE SEQUENCE Pro	UENCI) LEI) TYI) STI) TOI ECULI	E CHANGTH: PE: & RANDE POLOG E TYPE E DES	ARACT : 683 amino EDNES EY: 1 PE: 1 GCRII Gly 5	TERIS L ami D aci SS: s unknow Dept:	STICS ino a id singl swn ide Val	S: acids Le EQ II	O NO:	Asp 10	•				15	
2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034	(2)	(ii) (ii) (xi) Thr 1 Arg	SEQUENCE OF SEQUEN	UENCI) LET) TYI) STI) TOI ECULI UENCI Pro	E CHANGTH: PE: 6 RANDE POLOG E TYPE E DES Gln Asp 20	ARACT REDNES SY: 1 SCRII Gly 5	TERIS L ami D aci SS: s INNE PTION Glu Phe	STICS ino a id single swn ide Val	S: acids Le Q II Asp Pro	NO: Ala Leu 25	Asp 10 Met	Ile	Ala	Ser	Cys 30	15 Ser	Gly
2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035	(2)	(ii) (ii) (xi) Thr 1 Arg	SEQUENCE OF SEQUEN	UENCI DECULI Pro Pro Leu	E CHANGTH: PE: 6 RANDE POLOG E TYPE E DES	ARACT REDNES SY: 1 SCRII Gly 5	TERIS L ami D aci SS: s INNE PTION Glu Phe	STICS ino a id single swn ide Val	S: acids le Q II Asp Pro Ser	NO: Ala Leu 25	Asp 10 Met	Ile	Ala	Ser Asp	Cys 30	15 Ser	Gly
2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036	(2)	(ii) (ii) (xi) Thr 1 Arg	SEQUENCE OF SEQUEN	UENCI) LET) TYI) STI) TOI ECULI UENCI Pro	E CHANGTH: PE: 6 RANDE POLOG E TYPE E DES Gln Asp 20	ARACT REDNES SY: 1 SCRII Gly 5	TERIS L ami D aci SS: s Inkno PTION Glu Phe	STICS ino a id single swn ide Val	S: acids Le Q II Asp Pro	NO: Ala Leu 25	Asp 10 Met	Ile	Ala	Ser	Cys 30	15 Ser	Gly
2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037	(2)	(ii) (xi) Thr 1 Arg	SEQUENCE OF SEQUEN	UENCI DECULI Pro Pro Leu 35	E CHANGTH: PE: & RANDE POLOCE E TYPE Gln Asp 20 Glu	ARACT 683 683 684 687 687 687 687 687 687 687 687 687 687	TERIS L ami D aci SS: s unknot Depti	STICS ino a id single own ide Val Thr	S: acids le EQ II Asp Pro Ser 40	NO: Ala Leu 25 Glu	Asp 10 Met Glu	Ile Glu	Ala Glu	Ser Asp 45	Cys 30 Ala	15 Ser Pro	Gly Ala
2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2036 2037 2038	(2)	(ii) (xi) Thr 1 Arg	SEQUENCE OF SEQUEN	UENCI DECULI Pro Pro Leu 35	E CHANGTH: PE: 6 RANDE POLOG E TYPE Gln Asp 20	ARACT 683 683 684 687 687 687 687 687 687 687 687 687 687	TERIS L ami D aci SS: s unknot Depti	STICS ino a id sing own ide Val Thr Asn	S: acids le EQ II Asp Pro Ser 40	NO: Ala Leu 25 Glu	Asp 10 Met Glu	Ile Glu	Ala Glu Leu	Ser Asp 45	Cys 30 Ala	15 Ser Pro	Gly Ala
2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037	(2)	(ii) (xi) Thr 1 Arg	SEQUENCE OF SEQUEN	UENCI DECULI Pro Pro Leu 35	E CHANGTH: PE: & RANDE POLOCE E TYPE Gln Asp 20 Glu	ARACT 683 683 684 687 687 687 687 687 687 687 687 687 687	TERIS L ami D aci SS: s unknot Depti	STICS ino a id single own ide Val Thr	S: acids le EQ II Asp Pro Ser 40	NO: Ala Leu 25 Glu	Asp 10 Met Glu	Ile Glu	Ala Glu	Ser Asp 45	Cys 30 Ala	15 Ser Pro	Gly Ala

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2041	Asp	Arg	Thr	Gly	Glu	Thr	Ala	Leu	His	Leu	Ala	Ala	Arg	Tyr	Ser	Arg
2042	65					70					75					80
2043																
2044	Ser	Asp	Ala	Ala	Lys	Arg	Leu	Leu	Glu	Ala	Ser	Ala	Asp	Ala	Asn	Ile
2045					85					90					95	
2046																
2047	Gln	Asp	Asn	Met	Gly	Arq	Thr	Pro	Leu	His	Ala	Ala	Val	Ser	Ala	Asp
2048		-		100	-				105					110		-
2049																
2050	Ala	Gln	Glv	Val	Phe	Gln	Ile	Leu	Ile	Ara	Asn	Arg	Ala	Thr	Asp	Leu
2051			115					120		- 3		- 3	125			
2052																
2053	Asp	Ala	Ara	Met	His	Asp	Glv	Thr	Thr	Pro	Leu	Ile	Leu	Ala	Ala	Ara
2054		130	5				135					140				5
2055																
2056	Leu	Ala	Val	Glu	Glv	Met	Leu	Glu	Asp	Leu	Ile	Asn	Ser	His	Δla	Asp
2057	145	1114	• • • •	014	017	150		O-u	1101		155		501		mru	160
2058	-15															
2059	Val	Asn	Δla	Val	Δsn	Δsn	Len	Glv	Lve	Ser	Δla	T.e.11	Hie	Trn	Δla	Δla
2060	· u ·	11011	11±u	val	165	пор	Lcu	Cry		170	nia	Lcu	*****		175	nia
2061					105					-,0					1,5	
2062	Λla	Val	Agn	λan	Wa 1	λen	בומ	בומ	Val	Val	Leu	T.211	Luc	Λen	G1 17	λla
2063	AIA	Vai	ASII	180	vai	Asp	ΑΙα	Αια	185	vai	Leu	Leu	цуз	190	GIY	AIA
2064				100					103					190		
2065	7 an	Lys	Λan	Mo+	Cln.	Nan	7 an	Λ×α	C1,,	Clu	Thr	Dro	Lou	Dho	T 011	ת דת
2066	ASII	цуѕ	_	Mec	GIII	ASII	ASII	_	GIU	GIU	1111	PIO		FIIE	пец	AIA
			195					200					205			
2067	77-	7\ >===	a 1	a1	Com	TT	a1	III baa	77-	T	7707	T 0	T	7	TT-1 -	Dho
2068	AIA	Arg	GIU	GIY	Ser	TÀL		IIII	Ala	гуѕ	vaı		ьeu	Asp	птѕ	Pne
2069		210					215					220				
2070	77-	7.~~	7	7 ~~	т1.	mla sa	7	TT-1	M-+	7	7	T	Dage	7	7	T1.
2071		Asn	Arg	Asp	тте		Asp	nis	Met	Asp	_	ьeu	Pro	Arg	Asp	
2072	225					230					235					240
2073	77.	~1 <u>~</u>	C1	7 200	Mot	TT i a	TT-1 -	7	т1.	7707	7\ ><<	T	т	7	a1	TT
2074	AIA	Gln	GIU	Arg		пта	птѕ	Asp	тте		Arg	ьeu	ьeu	Asp		TYL
2075					245					250					255	
2076	7 ~~	т	7707	7 200	Com	Dwo	a1 =	T	TT-1 -	a1	71.	Deco	T	~1	a1	mb
2077	ASII	Leu	vai	_	Ser	PIO	GIII	ьeu		GIÀ	Ата	Pro	ьeu	_	GIY	IIII
2078				260					265					270		
2079	Dese	mla aa	T	0	D	D	T	a	a	D	7	a1	m	T	a1	0
2080	Pro	Thr	~	ser	Pro	Pro	ьeu		ser	Pro	ASII	GIĀ		Leu	GIY	ser
2081			275					280					285			
2082	T	T	D	a1	77-7	a1	a1	T	T	77-7	7	T	D	G	G	T
2083	Leu	Lys	Pro	GIY	vaı	GIN	_	ьуs	ьуs	vaı	Arg	_	Pro	ser	ser	ьуs
2084		290					295					300				
2085	~1 -			~	~1 -	~	-	a 1.		.	-		.			-
2086	_	Leu	Ата	cys	θŢЙ		ьуѕ	GLU	АТа	гуѕ	_	ьeu	ьуѕ	ΑΙα	arg	_
2087	305					310					315					320
2088	T	T	0	~ 1	7	a 1-	T	~ 1 -	~	т.	T	70	0	0	~ 1	N
2089	ьys	Lys	ser	GIN		GTA	ьys	GТĀ	cys		ьeu	Asp	ser	ser	_	Met
2090					325					330					335	
2091																

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2092 2093 2094	Leu	Ser	Pro	Val 340	Asp	Ser	Leu	Glu	Ser 345	Pro	His	Gly	Tyr	Leu 350	Ser	Asp
2095 2096 2097	Val	Ala	Ser 355	Pro	Pro	Leu	Leu	Pro 360	Ser	Pro	Phe	Gln	Gln 365	Ser	Pro	Ser
2098 2099 2100	Val	Pro 370	Leu	Asn	His	Leu	Pro 375	Gly	Met	Pro	Asp	Thr 380	His	Leu	Gly	Ile
2101 2102 2103	Gly 385	His	Leu	Asn	Val	Ala 390	Ala	Lys	Pro	Glu	Met 395	Ala	Ala	Leu	Gly	Gly 400
2104 2105 2106	Gly	Gly	Arg	Leu	Ala 405	Phe	Glu	Thr	Gly	Pro 410	Pro	Arg	Leu	Ser	His 415	Leu
2107 2108 2109	Pro	Val	Ala	Ser 420	Gly	Thr	Ser	Thr	Val 425	Leu	Gly	Ser	Ser	Ser 430	Gly	Gly
2110 2111 2112	Ala	Leu	Asn 435	Phe	Thr	Val	Gly	Gly 440	Ser	Thr	Ser	Leu	Asn 445	Gly	Gln	Cys
2113 2114 2115	Glu	Trp 450	Leu	Ser	Arg	Leu	Gln 455	Ser	Gly	Met	Val	Pro 460	Asn	Gln	Tyr	Asn
2116 2117 2118	Pro 465	Leu	Arg	Gly	Ser	Val 470	Ala	Pro	Gly	Pro	Leu 475	Ser	Thr	Gln	Ala	Pro 480
2119 2120 2121	Ser	Leu	Gln	His	Gly 485	Met	Val	Gly	Pro	Leu 490	His	Ser	Ser	Leu	Ala 495	Ala
2122 2123 2124	Ser	Ala	Leu	Ser 500	Gln	Met	Met	Ser	Tyr 505	Gln	Gly	Leu	Pro	Ser 510	Thr	Arg
2125 2126 2127	Leu	Ala	Thr 515	Gln	Pro	His	Leu	Val 520	Gln	Thr	Gln	Gln	Val 525	Gln	Pro	Gln
2128 2129 2130	Asn	Leu 530	Gln	Met	Gln	Gln	Gln 535	Asn	Leu	Gln	Pro	Ala 540	Asn	Ile	Gln	Gln
2131 2132 2133	Gln 545	Gln	Ser	Leu		Pro 550		Pro	Pro		Pro 555		Pro	His		Gly 560
2134 2135 2136	Val	Ser	Ser	Ala	Ala 565	Ser	Gly	His	Leu	Gly 570	Arg	Ser	Phe	Leu	Ser 575	Gly
2137 2138 2139	Glu	Pro	Ser	Gln 580	Ala	Asp	Val	Gln	Pro 585	Leu	Gly	Pro	Ser	Ser 590	Leu	Ala
2140 2141 2142	Val	His	Thr 595	Ile	Leu	Pro	Gln	Glu 600	Ser	Pro	Ala	Leu	Pro 605	Thr	Ser	Leu

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2143		Pro	Ser	Ser	Leu	Val	Pro	Pro	Val	Thr	Ala	Ala	Gln	Phe	Leu	Thr	Pro
2144			610					615					620				
2145																	
2146			Ser	Gln	His	Ser	Tyr	Ser	Ser	Pro	Val		Asn	Thr	Pro	Ser	His
2147		625					630					635					640
2148																	
2149		Gln	Leu	Gln	Val		Glu	His	Pro	Phe	Leu	Thr	Pro	Ser	Pro	Glu	Ser
2150						645					650					655	
2151							_	_						_			
2152		Pro	Asp	Gln		Ser	Ser	Ser	Ser		His	Ser	Asn	Val		Asp	\mathtt{Trp}
2153					660					665					670		
2154			~ 1	~1		•			_	1							
2155		ser	GIU	-	Val	ser	Ser	Pro		Thr							
2156				675					680								
2157	(0)	T. T. T. C. T.	3843 m		70D (FD 37										
2158	(2)	INFO	CMAT.	LON 1	OR S	SEQ .	LD NO):19	:								
2159		(4)	anor	יייייייי	- am	אור א מר		7mT (1									
2160 2161		(i)			E CHA					a _							
2162					PE: a				acit	15							
2163					RANDI				١٥								
2164					OLOC			_	re								
2165			(1)	101	ОПОС	31. (AIIAIIC	JWII									
2166		(ii)	MOL	eciii.	יעד ב	DE · r	nent i	ide									
2167		(11)	МОШ	30011		ъ. г	ocp c.	Luc									
2168																	
2169		(xi)	SEOU	JENCI	E DES	SCRII	TOITS	N: SI	EO II	ON C	:19:						
		(xi)	SEQU	JENCI	E DES	SCRII	OIT	N: SI	EQ II	ONO	:19:						
2169 2170												Ala	Leu	Leu	Ala	Leu	Trp
2169 2170 2171												Ala	Leu	Leu	Ala	Leu 15	Trp
2169 2170 2171 2172		Met				Arg					Trp	Ala	Leu	Leu	Ala		Trp
2169 2170 2171 2172 2173		Met 1	Pro	Ala	Leu	Arg 5	Pro	Ala	Leu	Leu	Trp 10						_
2169 2170 2171 2172 2173 2174		Met 1	Pro	Ala	Leu	Arg 5	Pro	Ala	Leu	Leu	Trp 10					15	_
2169 2170 2171 2172 2173 2174 2175		Met 1	Pro	Ala	Leu Ala	Arg 5	Pro	Ala	Leu	Leu Ala	Trp 10				Asp	15	_
2169 2170 2171 2172 2173 2174 2175 2176		Met 1 Leu	Pro Cys	Ala Cys	Leu Ala 20	Arg 5 Ala	Pro Pro	Ala Ala	Leu His	Leu Ala 25	Trp 10 Leu	Gln	Cys	Arg	Asp 30	15	Tyr
2169 2170 2171 2172 2173 2174 2175 2176 2177		Met 1 Leu	Pro Cys	Ala Cys	Leu Ala 20	Arg 5 Ala	Pro Pro	Ala Ala	Leu His	Leu Ala 25	Trp 10 Leu	Gln	Cys	Arg	Asp 30	15 Gly	Tyr
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178		Met 1 Leu Glu	Pro Cys Pro	Ala Cys Cys 35	Leu Ala 20 Val	Arg 5 Ala Asn	Pro Pro Glu	Ala Ala Gly	Leu His Met 40	Leu Ala 25 Cys	Trp 10 Leu Val	Gln Thr	Cys Tyr	Arg His 45	Asp 30 Asn	15 Gly Gly	Tyr Thr
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179		Met 1 Leu Glu	Pro Cys Pro	Ala Cys Cys 35	Leu Ala 20 Val	Arg 5 Ala Asn	Pro Pro Glu	Ala Ala Gly	Leu His Met 40	Leu Ala 25 Cys	Trp 10 Leu Val	Gln Thr	Cys Tyr	Arg His 45	Asp 30 Asn	15 Gly	Tyr Thr
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182		Met 1 Leu Glu	Pro Cys Pro	Ala Cys Cys 35	Leu Ala 20 Val	Arg 5 Ala Asn	Pro Pro Glu	Ala Ala Gly	Leu His Met 40	Leu Ala 25 Cys	Trp 10 Leu Val	Gln Thr	Cys Tyr	Arg His 45	Asp 30 Asn	15 Gly Gly	Tyr Thr
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181		Met 1 Leu Glu Gly	Pro Cys Pro Tyr 50	Ala Cys Cys 35 Cys	Leu Ala 20 Val Lys	Arg 5 Ala Asn Cys	Pro Pro Glu Pro	Ala Ala Gly Glu 55	Leu His Met 40 Gly	Leu Ala 25 Cys Phe	Trp 10 Leu Val Leu	Gln Thr	Cys Tyr Glu 60	Arg His 45 Tyr	Asp 30 Asn Cys	15 Gly Gly Gln	Tyr Thr His
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184		Met 1 Leu Glu Gly	Pro Cys Pro Tyr 50	Ala Cys Cys 35 Cys	Leu Ala 20 Val Lys	Arg 5 Ala Asn Cys	Pro Pro Glu Pro Lys	Ala Ala Gly Glu 55	Leu His Met 40 Gly	Leu Ala 25 Cys Phe	Trp 10 Leu Val Leu	Gln Thr Gly Asn	Cys Tyr Glu 60	Arg His 45 Tyr	Asp 30 Asn Cys	15 Gly Gly	Tyr Thr His
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185		Met 1 Leu Glu Gly	Pro Cys Pro Tyr 50	Ala Cys Cys 35 Cys	Leu Ala 20 Val Lys	Arg 5 Ala Asn Cys	Pro Pro Glu Pro	Ala Ala Gly Glu 55	Leu His Met 40 Gly	Leu Ala 25 Cys Phe	Trp 10 Leu Val Leu	Gln Thr	Cys Tyr Glu 60	Arg His 45 Tyr	Asp 30 Asn Cys	15 Gly Gly Gln	Tyr Thr His
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186		Met 1 Leu Glu Gly Arg 65	Pro Cys Pro Tyr 50 Asp	Ala Cys Cys 35 Cys	Leu Ala 20 Val Lys Cys	Arg 5 Ala Asn Cys Glu	Pro Glu Pro Lys	Ala Gly Glu 55 Asn	Leu His Met 40 Gly	Leu Ala 25 Cys Phe	Trp 10 Leu Val Leu Gln	Gln Thr Gly Asn 75	Cys Tyr Glu 60 Gly	Arg His 45 Tyr	Asp 30 Asn Cys	Gly Gly Gln Cys	Tyr Thr His
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187		Met 1 Leu Glu Gly Arg 65	Pro Cys Pro Tyr 50 Asp	Ala Cys Cys 35 Cys	Leu Ala 20 Val Lys Cys	Arg 5 Ala Asn Cys Glu Leu	Pro Glu Pro Lys	Ala Gly Glu 55 Asn	Leu His Met 40 Gly	Leu Ala 25 Cys Phe	Trp 10 Leu Val Leu Gln	Gln Thr Gly Asn 75	Cys Tyr Glu 60 Gly	Arg His 45 Tyr	Asp 30 Asn Cys	Gly Gln Cys Gly	Tyr Thr His
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188		Met 1 Leu Glu Gly Arg 65	Pro Cys Pro Tyr 50 Asp	Ala Cys Cys 35 Cys	Leu Ala 20 Val Lys Cys	Arg 5 Ala Asn Cys Glu	Pro Glu Pro Lys	Ala Gly Glu 55 Asn	Leu His Met 40 Gly	Leu Ala 25 Cys Phe	Trp 10 Leu Val Leu Gln	Gln Thr Gly Asn 75	Cys Tyr Glu 60 Gly	Arg His 45 Tyr	Asp 30 Asn Cys	Gly Gly Gln Cys	Tyr Thr His
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188		Met 1 Leu Glu Gly Arg 65 Ala	Pro Cys Pro Tyr 50 Asp	Ala Cys Cys 35 Cys Pro	Leu Ala 20 Val Lys Cys Met	Arg 5 Ala Asn Cys Glu Leu 85	Pro Glu Pro Lys 70 Gly	Ala Gly Glu 55 Asn	Leu His Met 40 Gly Arg	Leu Ala 25 Cys Phe Cys	Trp 10 Leu Val Leu Gln Cys 90	Gln Thr Gly Asn 75 Arg	Cys Tyr Glu 60 Gly Cys	Arg His 45 Tyr Gly	Asp 30 Asn Cys Thr	Gly Gln Cys Gly 95	Tyr Thr His Val 80 Phe
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190		Met 1 Leu Glu Gly Arg 65 Ala	Pro Cys Pro Tyr 50 Asp	Ala Cys Cys 35 Cys Pro	Leu Ala 20 Val Lys Cys Met Asp	Arg 5 Ala Asn Cys Glu Leu 85	Pro Glu Pro Lys 70 Gly	Ala Gly Glu 55 Asn	Leu His Met 40 Gly Arg	Leu Ala 25 Cys Phe Cys Thr	Trp 10 Leu Val Leu Gln Cys 90	Gln Thr Gly Asn 75 Arg	Cys Tyr Glu 60 Gly Cys	Arg His 45 Tyr Gly	Asp 30 Asn Cys Thr	Gly Gln Cys Gly	Tyr Thr His Val 80 Phe
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191		Met 1 Leu Glu Gly Arg 65 Ala	Pro Cys Pro Tyr 50 Asp	Ala Cys Cys 35 Cys Pro	Leu Ala 20 Val Lys Cys Met	Arg 5 Ala Asn Cys Glu Leu 85	Pro Glu Pro Lys 70 Gly	Ala Gly Glu 55 Asn	Leu His Met 40 Gly Arg	Leu Ala 25 Cys Phe Cys	Trp 10 Leu Val Leu Gln Cys 90	Gln Thr Gly Asn 75 Arg	Cys Tyr Glu 60 Gly Cys	Arg His 45 Tyr Gly	Asp 30 Asn Cys Thr	Gly Gln Cys Gly 95	Tyr Thr His Val 80 Phe
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190		Met 1 Leu Glu Gly Arg 65 Ala	Pro Cys Pro Tyr 50 Asp Gln	Ala Cys Cys 35 Cys Pro Ala Glu	Leu Ala 20 Val Lys Cys Met Asp 100	Arg 5 Ala Asn Cys Glu Leu 85 Cys	Pro Glu Pro Lys 70 Gly Gln	Ala Gly Glu 55 Asn Lys	Leu His Met 40 Gly Arg Ala Ser	Leu Ala 25 Cys Phe Cys Thr	Trp 10 Leu Val Leu Gln Cys 90 Ser	Gln Thr Gly Asn 75 Arg	Cys Tyr Glu 60 Gly Cys	Arg His 45 Tyr Gly Ala Cys	Asp 30 Asn Cys Thr Ser	Gly Gln Cys Gly 95	Tyr Thr His Val 80 Phe

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2194			115					120					125			
2195	_											_				
2196	Tyr		Cys	Thr	Cys	GIn		GLY	Phe	Thr	GLY		Glu	Cys	Gln	Trp
2197		130					135					140				
2198	_		_							_		_				
2199		Asp	Ala	Cys	Leu		His	Pro	Cys	Ala	Asn	Gly	Ser	Thr	Cys	Thr
2200	145					150					155					160
2201																
2202	Thr	Val	Ala	Asn		Phe	Ser	Cys	Lys	Cys	Leu	Thr	Gly	Phe	Thr	Gly
2203					165					170					175	
2204																
2205	Gln	Lys	Cys	Glu	Thr	Asp	Val	Asn	Glu	Cys	Asp	Ile	Pro	Gly	His	Cys
2206				180					185					190		
2207																
2208	Gln	His	Gly	Gly	Thr	Cys	Leu	Asn	Leu	Pro	${ t Gly}$	Ser	Tyr	Gln	Cys	Gln
2209			195					200					205			
2210																
2211	Cys	Pro	Gln	Gly	Phe	Thr	Gly	Gln	Tyr	Cys	Asp	Ser	Leu	Tyr	Val	Pro
2212		210					215					220				
2213																
2214	Cys	Ala	Pro	Ser	Pro	Cys	Val	Asn	Gly	Gly	Thr	Cys	Arg	Gln	Thr	Gly
2215	225					230					235					240
2216																
2217	Asp	Phe	Thr	Phe	Glu	Cys	Asn	Cys	Leu	Pro	Gly	Phe	Glu	Gly	Ser	Thr
2218					245					250					255	
2219																
2220	Cys	Glu	Arg	Asn	Ile	Asp	Asp	Cys	Pro	Asn	His	Arg	Cys	Gln	Asn	Gly
2221				260					265					270		
2222																
2223	Gly	Val	Cys	Val	Asp	Gly	Val	Asn	Thr	Tyr	Asn	Cys	Arg	Cys	Pro	Pro
2224	_		275		_	_		280		-		_	285	_		
2225																
2226	Gln	Trp	Thr	Gly	Gln	Phe	Cys	Thr	Glu	Asp	Val	Asp	Glu	Cys	Leu	Leu
2227		290					295					300				
2228																
2229	Gln	Pro	Asn	Ala	Cys	Gln	Asn	Gly	Gly	Thr	Cys	Ala	Asn	Arg	Asn	Gly
2230	305					310		_	_		315			_		320
2231																
2232	Gly	Tyr	Gly	Cys	Val	Cys	Val	Asn	Gly	Trp	Ser	Gly	Asp	Asp	Cys	Ser
2233		_	_		325				_	330		_	_	_	335	
2234																
2235	Glu	Asn	Ile	Asp	Asp	Cys	Ala	Phe	Ala	Ser	Cys	Thr	Pro	Gly	Ser	Thr
2236				340	_	_			345		_			350		
2237																
2238	Cys	Ile	Asp	Arg	Val	Ala	Ser	Phe	Ser	Cys	Met	Cys	Pro	Glu	Gly	Lys
2239	-		355					360		-		-	365		-	_
2240																
2241	Ala	Gly	Leu	Leu	Cys	His	Leu	Asp	Asp	Ala	Cys	Ile	Ser	Asn	Pro	Cys
2242		370			-		375	_	_		-	380				_
2243																
2244	His	Lys	Gly	Ala	Leu	Cys	Asp	Thr	Asn	Pro	Leu	Asn	Gly	Gln	Tyr	Ile

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2245 2246	385					390					395					400
2247	Cvs	Thr	Cvs	Pro	Gln	Glv	Tvr	Lvs	Glv	Ala	Asp	Cvs	Thr	Glu	Asp	Val
2248	-7.5		0,70		405	1	-1-	-75		410		0,5			415	Val
2249																
2250	Asp	Glu	Cvs	Ala	Met	Ala	Asn	Ser	Asn	Pro	Cvs	Glu	His	Ala	Gly	Lvs
2251			-1-	420					425		-1-			430	1	-1-
2252														-50		
2253	Cvs	Val	Asn	Thr	Asp	Glv	Ala	Phe	His	Cvs	Glu	Cvs	Leu	Lvs	Gly	Tvr
2254	- 2		435			2		440		-1-		-1 -	445	-1 -	1	- 1 -
2255																
2256	Ala	Glv	Pro	Ara	Cvs	Glu	Met	Asp	Tle	Asn	Glu	Cvs	His	Ser	Asp	Pro
2257		450			-7-		455					460		501	1101	
2258																
2259	Cvs	Gln	Asn	Asp	Ala	Thr	Cvs	Leu	Asp	Lvs	Tle	Glv	Glv	Phe	Thr	Cvs
2260	465					470	-72		1101	-7-	475	1				480
2261																100
2262	Leu	Cvs	Met	Pro	Glv	Phe	Lvs	Glv	Val	His	Cvs	Glu	Leu	Glu	Ile	Asn
2263		- 2 -			485		-1 -	1		490	-1-				495	
2264																
2265	Glu	Cvs	Gln	Ser	Asn	Pro	Cvs	Val	Asn	Asn	Glv	Gln	Cvs	Val	Asp	Lvs
2266		-1-		500			-7-		505		- -1		0,72	510	P	-15
2267																
2268	Val	Asn	Arq	Phe	Gln	Cvs	Leu	Cvs	Pro	Pro	Glv	Phe	Thr	Glv	Pro	Val
2269			515			•		520			-		525	2		
2270																
2271	Cys	Gln	Ile	Asp	Ile	Asp	Asp	Cys	Ser	Ser	Thr	Pro	Cys	Leu	Asn	Glv
2272	-	530		-		-	535	•				540	•			•
2273																
2274	Ala	Lys	Cys	Ile	Asp	His	Pro	Asn	Gly	Tyr	Glu	Cys	Gln	Cys	Ala	Thr
2275	545	_	-		_	550			•	•	555	•		•		560
2276																
2277	Gly	Phe	Thr	Gly	Val	Leu	Cys	Glu	Glu	Asn	Ile	Asp	Asn	Cys	Asp	Pro
2278					565		-			570		_		-	575	
2279																
2280	Asp	Pro	Cys	His	His	Gly	Gln	Cys	Gln	Asp	Gly	Ile	Asp	Ser	Tyr	Thr
2281				580					585					590		
2282																
2283	Cys	Ile	Cys	Asn	Pro	Gly	Tyr	Met	Gly	Ala	Ile	Cys	Ser	Asp	Gln	Ile
2284			595					600					605			
2285																
2286	Asp	Glu	Cys	Tyr	Ser	Ser	${\tt Pro}$	Cys	Leu	Asn	Asp	Gly	Arg	Cys	Ile	Asp
2287		610					615					620				
2288																
2289		Val	Asn	Gly	Tyr		Cys	Asn	Cys	Gln	Pro	Gly	Thr	Ser	Gly	
2290	625					630					635					640
2291			_	_						_					_	
2292	Asn	Cys	Glu	Ile		Phe	Asp	Asp	Cys		Ser	Asn	Pro	Суз	Ile	His
2293					645					650					655	
2294	a 3	~ 7	a -			~ 7	~7	_	_	_		_		_	~ .	_
2295	GТĀ	тте	cys	met	Asp	GTĀ	тте	Asn	Arg	Tyr	ser	Cys	val	cys	Ser	Pro

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2296				660					665					670		
2297 2298	Glv	Dhe	Thr	Glaz	Gln	Λrα	Carc	λan	Tla	7) cm	Tla	Nan	C1,,	Czza	Ala	Cor
2299	OI y	1110	675	O _T y	GIII	Arg	Cys	680	110	Asp	110	тэр	685	Суз	Ата	261
2300			• • •										000			
2301	Asn	Pro	Cvs	Arq	Lvs	Glv	Ala	Thr	Cvs	Ile	Asn	Glv	Val	Asn	Gly	Phe
2302		690					695		-1-			700		-	1	
2303																
2304	Arq	Cys	Ile	Cys	Pro	Glu	Gly	Pro	His	His	Pro	Ser	Cvs	Tvr	Ser	Gln
2305	705	•		•		710	_				715		4	-	_	720
2306																
2307	Val	Asn	Glu	Cys	Leu	Ser	Asn	Pro	Cys	Ile	His	Gly	Asn	Cys	Thr	Gly
2308				-	725				-	730		•		•	735	-
2309																
2310	Gly	Leu	Ser	Gly	Tyr	Lys	Cys	Leu	Cys	Asp	Ala	Gly	Trp	Val	Gly	Ile
2311	_			740			_		745	_		_		750	_	
2312																
2313	Asn	Cys	Glu	Val	Asp	Lys	Asn	Glu	Cys	Leu	Ser	Asn	Pro	Cys	Gln	Asn
2314			755					760					765			
2315																
2316	Gly	Gly	Thr	Cys	Asp	Asn	Leu	Val	Asn	Gly	Tyr	Arg	Cys	Thr	Cys	Lys
2317		770					775					780				
2318																
2319	Lys	Gly	Phe	Lys	Gly	Tyr	Asn	Cys	Gln	Val	Asn	Ile	Asp	Glu	Cys	Ala
2320	785					790					795					800
2321																
2322	Ser	Asn	Pro	Cys	Leu	Asn	Gln	Gly	Thr	Cys	Phe	Asp	Asp	Ile	Ser	Gly
2323					805					810					815	
2324																
2325	Tyr	Thr	Cys		Cys	Val	Leu	Pro	_	Thr	Gly	Lys	Asn	Cys	Gln	Thr
2326				820					825					830		
2327							_	_	_	_	~ 7	_				_
2328	Val	Leu		Pro	Cys	Ser	Pro		Pro	Cys	GIu	Asn		Ala	Val	Cys
2329			835					840					845			
2330	T ~	a1	Com	Dwa	7	Dha	a1	C	m	mb	a	T	a	77.	D	a 1
2331 2332	гуѕ		ser	Pro	Asn	Pne		ser	Tyr	Thr	Cys		Cys	Ala	Pro	GIY
2333		850					855					860				
2334	Trn	Gln	G1 v	Gln	7) ra	Cvc	Thr	Tla	Λan	т1а	Nan	G1,1	Cva	Tla	Ser	Larg
2335	865	GIII	СТУ	GIII	Arg	870	1111	116	Asp	116	875	Giu	Cys	TTE	SET	880 880
2336	003					070					0/5					000
2337	Pro	Cva	Met	Δan	Hig	Glv	T.e.11	Cva	Hig	Δan	Thr	Gln	Glv	Ser	Tyr	Met
2338		Cyb		ADII	885	017	LCu	Cyb	1110	890		0111	O- y	501	895	
2339					000					030					0,00	
2340	Cvs	Glu	Cvs	Pro	Pro	Glv	Phe	Ser	Glv	Met.	Asp	Cvs	Glu	Glu	Asp	Ile
2341	-1-		-1.5	900		1			905		<u>-</u> -	-15		910	<u>r</u>	
2342																
2343	Asp	Asp	Cys	Leu	Ala	Asn	Pro	Cvs	Gln	Asn	Glv	Glv	Ser	Cvs	Met	Asp
2344	- T -	- 12	915					920			-1	- 2	925	1-		1
2345																
2346	Gly	Val	Asn	Thr	Phe	Ser	Cys	Leu	Cys	Leu	Pro	Gly	Phe	Thr	Gly	Asp

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2347		930					935					940				
2348		,,,,					,,,,					210				
2349	Lys	Cys	Gln	Thr	Asp	Met	Asn	Glu	Cys	Leu	Ser	Glu	Pro	Cys	Lys	Asn
2350	945					950			_		955			-		960
2351																
2352	Gly	Gly	Thr	Cys	Ser	Asp	Tyr	Val	Asn	Ser	Tyr	Thr	Cys	Lys	Cys	Gln
2353					965					970			_	-	975	
2354																
2355	Ala	Gly	Phe	Asp	Gly	Val	His	Cys	Glu	Asn	Asn	Ile	Asn	Glu	Cys	Thr
2356				980					985					990		
2357																
2358	Glu	Ser	Ser	Cys	Phe	Asn	Gly	Gly	Thr	Cys	Val	Asp	Gly	Ile	Asn	Ser
2359			995					1000)				1005	5		
2360																
2361	Phe	Ser	Cys	Leu	Cys	Pro	Val	Gly	Phe	Thr	Gly	Ser	Phe	Cys	Leu	His
2362		1010)				1015	5				1020)			
2363																
2364			Asn	Glu	Cys	Ser	Ser	His	Pro	Cys	Leu	Asn	Glu	Gly	Thr	Cys
2365	1025	5				1030)				1035	5				1040
2366																
2367	Val	Asp	Gly	Leu	Gly	Thr	Tyr	Arg	Cys	Ser	Cys	Pro	Leu	Gly	Tyr	Thr
2368					1045	5				1050)				1055	5
2369																
2370	Gly	Lys	Asn	Cys	Gln	Thr	Leu	Val	Asn	Leu	Cys	Ser	Arg	Ser	Pro	Cys
2371				1060)				1065	5				1070)	
2372																
2373	Lys	Asn	Lys	Gly	Thr	Cys	Val	Gln	Lys	Lys	Ala	Glu	Ser	Gln	Cys	Leu
2374			1075	5				1080)				1085	5		
2375																
2376																
23/6	Cys	Pro	Ser	Gly	Trp	Ala	Gly	Ala	Tyr	Cys	Asp	Val	Pro	Asn	Val	Ser
2377	Cys	Pro 1090		Gly	Trp	Ala	Gly 1095		Tyr	Cys	Asp	Val 1100		Asn	Val	Ser
		1090)				1095	5				1100)			
2377 2378 2379	Cys	1090 Asp)				1095	5		Cys		1100)			
2377 2378 2379 2380		1090 Asp)				1095 Arg	5				1100 Val)			
2377 2378 2379 2380 2381	Cys 1105	1090 Asp) Ile	Ala	Ala	Ser 111(1095 Arg)	Arg	Gly	Val	Leu 1115	1100 Val) Glu	His	Leu	Cys 1120
2377 2378 2379 2380 2381 2382	Cys 1105	1090 Asp) Ile	Ala	Ala Val	Ser 1110 Cys	1095 Arg)	Arg	Gly	Val Gly	Leu 1115 Asn	1100 Val) Glu	His	Leu	Cys 1120
2377 2378 2379 2380 2381 2382 2383	Cys 1105	1090 Asp) Ile	Ala	Ala	Ser 1110 Cys	1095 Arg)	Arg	Gly	Val	Leu 1115 Asn	1100 Val) Glu	His	Leu	Cys 1120 Gln
2377 2378 2379 2380 2381 2382 2383 2384	Cys 1105 Gln	1090 Asp His	Ile Ser	Ala Gly	Ala Val 1125	Ser 1110 Cys	1099 Arg) Ile	Arg Asn	Gly Ala	Val Gly 1130	Leu 1115 Asn)	1100 Val 5 Thr	Glu His	His Tyr	Leu Cys 1135	Cys 1120 Gln
2377 2378 2379 2380 2381 2382 2383 2384 2385	Cys 1105 Gln	1090 Asp His	Ile Ser	Ala Gly Gly	Ala Val 1125 Tyr	Ser 1110 Cys	1099 Arg) Ile	Arg Asn	Gly Ala Tyr	Val Gly 1130 Cys	Leu 1115 Asn)	1100 Val 5 Thr	Glu His	His Tyr Leu	Leu Cys 1135	Cys 1120 Gln
2377 2378 2379 2380 2381 2382 2383 2384 2385 2386	Cys 1105 Gln	1090 Asp His	Ile Ser	Ala Gly	Ala Val 1125 Tyr	Ser 1110 Cys	1099 Arg) Ile	Arg Asn	Gly Ala	Val Gly 1130 Cys	Leu 1115 Asn)	1100 Val 5 Thr	Glu His	His Tyr	Leu Cys 1135	Cys 1120 Gln
2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387	Cys 1105 Gln Cys	Asp His	Ile Ser Leu	Ala Gly Gly 1140	Ala Val 1125 Tyr	Ser 1110 Cys Thr	Arg) Ile	Arg Asn Ser	Gly Ala Tyr 1145	Val Gly 1130 Cys	Leu 1115 Asn) Glu	Val Thr	Glu His Gln	His Tyr Leu 1150	Leu Cys 1135 Asp	Cys 1120 Gln Glu
2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388	Cys 1105 Gln Cys	Asp His	Ile Ser Leu Ser	Ala Gly Gly 1140 Asn	Ala Val 1125 Tyr	Ser 1110 Cys Thr	Arg) Ile	Arg Asn Ser	Gly Ala Tyr 1145	Val Gly 1130 Cys	Leu 1115 Asn) Glu	Val Thr	Glu His Gln Ser	His Tyr Leu 1150	Leu Cys 1135 Asp	Cys 1120 Gln Glu
2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389	Cys 1105 Gln Cys	Asp His	Ile Ser Leu	Ala Gly Gly 1140 Asn	Ala Val 1125 Tyr	Ser 1110 Cys Thr	Arg) Ile	Arg Asn Ser	Gly Ala Tyr 1145	Val Gly 1130 Cys	Leu 1115 Asn) Glu	Val Thr	Glu His Gln	His Tyr Leu 1150	Leu Cys 1135 Asp	Cys 1120 Gln Glu
2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390	Cys 1105 Gln Cys	Asp His Pro	Ile Ser Leu Ser	Gly Gly 1140 Asn	Ala Val 1125 Tyr) Pro	Ser 1110 Cys Thr	Arg) Ile Gly	Arg Asn Ser His	Gly Ala Tyr 1145 Gly	Gly 1130 Cys Ala	Leu 1115 Asn) Glu Thr	Val Thr Glu	Glu His Gln Ser	His Tyr Leu 1150 Asp	Cys 1135 Asp	Cys 1120 Gln Glu Ile
2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391	Cys 1105 Gln Cys	Asp His Pro Ala	Ile Ser Leu Ser 1155	Gly Gly 1140 Asn	Ala Val 1125 Tyr) Pro	Ser 1110 Cys Thr	Arg Ile Gly Gln Cys	Arg Asn Ser His 1160	Gly Ala Tyr 1145 Gly	Val Gly 1130 Cys	Leu 1115 Asn) Glu Thr	Val Thr Glu Cys	Glu His Gln Ser 1165	His Tyr Leu 1150 Asp	Cys 1135 Asp	Cys 1120 Gln Glu Ile
2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392	Cys 1105 Gln Cys	Asp His Pro	Ile Ser Leu Ser 1155	Gly Gly 1140 Asn	Ala Val 1125 Tyr) Pro	Ser 1110 Cys Thr	Arg) Ile Gly	Arg Asn Ser His 1160	Gly Ala Tyr 1145 Gly	Gly 1130 Cys Ala	Leu 1115 Asn) Glu Thr	Val Thr Glu	Glu His Gln Ser 1165	His Tyr Leu 1150 Asp	Cys 1135 Asp	Cys 1120 Gln Glu Ile
2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393	Cys 1105 Gln Cys Cys	Asp His Pro Ala	Ile Ser Leu Ser 1155	Ala Gly Gly 1140 Asn Arg	Val 1125 Tyr Pro	Ser 1110 Cys Thr Cys	Ile Gly Gln Cys 1175	Arg Asn Ser His 1160	Gly Ala Tyr 1145 Gly Pro	Gly 1130 Cys Ala	Leu 1115 Asn Glu Thr	Val Thr Glu Cys Gln 1180	Glu His Gln Ser 1165	His Tyr Leu 1150 Asp	Cys 1135 Asp Phe	Cys 1120 Gln Glu Ile
2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394	Cys 1105 Gln Cys Cys Gly	Asp His Pro Ala Gly 1170	Ile Ser Leu Ser 1155	Ala Gly Gly 1140 Asn Arg	Val 1125 Tyr Pro	Ser 1110 Cys Thr Cys Glu	Arg Ile Gly Gln Cys 1175	Arg Asn Ser His 1160	Gly Ala Tyr 1145 Gly Pro	Gly 1130 Cys Ala	Leu 1119 Asn Glu Thr Tyr	Val Thr Glu Cys Gln 1180	Glu His Gln Ser 1165	His Tyr Leu 1150 Asp	Cys 1135 Asp Phe	Cys 1120 Gln Glu Ile Cys
2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395	Cys 1105 Gln Cys Cys	Asp His Pro Ala Gly 1170	Ile Ser Leu Ser 1155	Ala Gly Gly 1140 Asn Arg	Val 1125 Tyr Pro	Ser 1110 Cys Thr Cys	Arg Ile Gly Gln Cys 1175	Arg Asn Ser His 1160	Gly Ala Tyr 1145 Gly Pro	Gly 1130 Cys Ala	Leu 1115 Asn Glu Thr	Val Thr Glu Cys Gln 1180	Glu His Gln Ser 1165	His Tyr Leu 1150 Asp	Cys 1135 Asp Phe	Cys 1120 Gln Glu Ile
2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394	Cys 1105 Gln Cys Cys Gly Glu 1185	Asp His Pro Ala Gly 1170	Ser Leu Ser 1155 Tyr	Gly Gly 1140 Asn Arg	Val 1125 Tyr Pro Cys	Ser 1110 Cys Thr Cys Glu Glu 1190	Arg Ile Gly Gln Cys 1175	Arg Asn Ser His 1160 Val Gln	Gly Ala Tyr 1145 Gly Pro Asn	Gly 1130 Cys Ala	Leu 1115 Asn Glu Thr Tyr Pro 1195	Val Thr Glu Cys Gln 1180	Glu His Gln Ser 1169 Gly Gln	His Tyr Leu 1150 Asp Val	Cys 1135 Asp Phe Asn	Cys 1120 Gln Glu Ile Cys

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2398					1205	5				121	0				121	5
2399 2400	Thr	7 ~~	C112	Leu	T 011	Czzo	C111	C1.,	7 an	T1.	7.00	7.00	Cara	777.	7. ~~~	C1
2401	1111	Arg	Gly	122		Cys	Giu	GIU	122!		Asp	Asp	Cys	123	_	GIY
2402				122	J				122	3				1231	J	
2402	Dro	Hic	Cvc	Leu	Λen	Glv	Clv	Gl n	Cva	Mot	7 an	7.20	Tlo	Clv	C111	T1.22
2404	FIO	1113	123!		ASII	GIY	GIY	124	_	Mec	Asp	Arg	124	-	GIY	ıyı
2405			120.	,				127	,				124.	,		
2406	Ser	Cve	Δrα	Cys	T.e.11	Dro	Glv	Dhe	Δla	Glv	Glu	Δrα	Cve	Glu	Glv	λen
2407	DCI	1250	_	Cys	шси	110	125		AIG	Cly	GIU	126	_	GIU	СТУ	Asp
2408		123	•				125.	•				120	•			
2409	Tle	Δsn	Glu	Cys	T.eu	Ser	Δsn	Pro	Cvs	Ser	Ser	Glu	Glv	Ser	T.e.11	Δsn
2410	126		014	Cyb	пси	1270		110	Cys	DCI	127		CIY	DCI	пси	1280
2411	120.					12/	•					•				1200
2412	Cvs	Tle	Gln	Leu	Thr	Δsn	Asn	Туг	Len	Cvs	Val	Cva	Δrα	Ser	Δla	Dhe
2413	0,0		0111	200	1285		1101	-1-	шси	129		C , 5	9	501	129	
2414					120.	•					•				12).	•
2415	Thr	Glv	Ara	His	Cvs	Glu	Thr	Phe	Val	Asp	Val	Cvs	Pro	Gln	Met.	Pro
2416		0-1	9	1300	-				130	_		0,0		1310		
2417					-					-						
2418	Cvs	Leu	Asn	Gly	Glv	Thr	Cvs	Ala	Val	Ala	Ser	Asn	Met	Pro	Asp	Glv
2419	-1		131!		1		-1-	1320					132			1
2420													_			
2421	Phe	Ile	Cys	Arg	Cys	Pro	Pro	Gly	Phe	Ser	Gly	Ala	Arq	Cvs	Gln	Ser
2422		1330	_		-		1335	-			-	1340	_	-2		
2423																
2424	Ser	Cys	Gly	Gln	Val	Lys	Cys	Arq	Lvs	Gly	Glu	Gln	Cvs	Val	His	Thr
2425	1345	_	-			1350	_	,	-	•	135		-			1360
2426																
2427	Ala	Ser	Gly	Pro	Arg	Cys	Phe	Cys	Pro	Ser	Pro	Arg	Asp	Cys	Glu	Ser
2428			_		1365	5		_		137	0	_	_	_	1375	5
2429																
2430	Gly	Cys	Ala	Ser	Ser	Pro	Cys	Gln	His	Gly	Gly	Ser	Cys	His	Pro	Gln
2431				1380)				138	5				1390)	
2432																
2433	Arg	Gln	Pro	Pro	Tyr	Tyr	Ser	Cys	Gln	Cys	Ala	Pro	Pro	Phe	Ser	Gly
2434			139	5				1400)				140	5		
2435																
2436	Ser	Arg	Cys	Glu	Leu	Tyr	Thr	Ala	Pro	Pro	Ser	Thr	Pro	Pro	Ala	Thr
2437		1410)				1415	5				1420)			
2438																
2439	_		Ser	Gln	${ t Tyr}$	Cys	Ala	Asp	Lys	Ala	Arg	Asp	Gly	Val	Cys	Asp
2440	1425	5				1430)				143	5				1440
2441	_	_					_		_			_	_			
2442	Glu	Ala	Cys	Asn			Ala	Cys	Gln	_	_	Gly	Gly	Asp	_	
2443					1445	5				145	0				145	5
2444	_	_,		~-	_	_	_		_	_	_	_	_	_	_	_
2445	Leu	Thr	Met	Glu		Pro	Trp	Ala		_	Ser	Ser	Pro			Cys
2446				1460	J				146	5				1470)	
2447	m.	_	_		_	_	a -	~	_	~ 7	_	-	_			~ 7
2448	rrp	Asp	Tyr	Ile	Asn	Asn	GIN	Cys	Asp	GIU	ьeu	Cys	Asn	Thr	٧al	GIU

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2449			1479	5				148	0				148	5		
2450																
2451	Cys			Asp	Asn	Phe	Glu	Cys	Gln	Gly	Asn	Ser	Lys	Thr	Cys	Lys
2452		1490)				149	5				1500)			
2453										1						
2454	Tyr	Asp	Lys	Tyr	Cys	Ala	Asp	His	Phe	Lys	Asp	Asn	His	Cys	Asn	Gln
2455	1509	5				1510)				151	5				1520
2456																
2457	Gly	Cys	Asn	Ser	Glu	Glu	Cys	Gly	Trp	Asp	Gly	Leu	Asp	Cys	Ala	Ala
2458					1525	5				1530)				153	5
2459																
2460	Asp	Gln	Pro	Glu	Asn	Leu	Ala	Glu	Gly	Thr	Leu	Val	Ile	Val	Val	Leu
2461				1540)				154	5				1550)	
2462																
2463	Met	Pro	Pro	Glu	Gln	Leu	Leu	Gln	Asp	Ala	Arg	Ser	Phe	Leu	Arg	Ala
2464			1559	5				156	0 _				156	5	_	
2465																
2466	Leu	Gly	Thr	Leu	Leu	His	Thr	Asn	Leu	Arg	Ile	Lys	Arg	Asp	Ser	Gln
2467		1570)				1579	5		_		1580	o _	_		
2468																
2469	Gly	Glu	Leu	Met	Val	Tyr	Pro	Tyr	Tyr	Gly	Glu	Lys	Ser	Ala	Ala	Met
2470	1589					1590		_	-	_	159	_				1600
2471																
2472	Lys	Lys	Gln	Arg	Met	Thr	Arg	Arg	Ser	Leu	Pro	Gly	Glu	Gln	Glu	Gln
2473	_	_		_	1609	5	_	_		1610)	_			1619	5
2474																
2475	Glu	Val	Ala	Gly	Ser	Lys	Val	Phe	Leu	Glu	Ile	Asp	Asn	Arq	Gln	Cys.
2476				1620		•			162			-		1630		•
2477																
2478	Val	Gln	Asp	Ser	Asp	His	Cys	Phe	Lys	Asn	Thr	Asp	Ala	Ala	Ala	Ala
2479			1639		_		-	1640	_			-	164			
2480																
2481	Leu	Leu	Ala	Ser	His	Ala	Ile	Gln	Gly	Thr	Leu	Ser	Tyr	Pro	Leu	Val
2482		1650					1659		-			1660	_			
2483																
2484	Ser	Val	Val	Ser	Glu	Ser	Leu	Thr	Pro	Glu	Arg	Thr	Gln	Leu	Leu	Tyr
2485	1669					1670					1679					1680
2486																
2487	Leu	Leu	Ala	Val	Ala	Val	Val	Ile	Ile	Leu	Phe	Ile	Ile	Leu	Leu	Gly
2488					1689					1690					1699	
2489																
2490	Val	Ile	Met	Ala	Lys	Arq	Lys	Arq	Lys	His	Gly	Ser	Leu	Trp	Leu	Pro
2491				1700	_		-	_	1709		-			171		
2492																
2493	Glu	Gly	Phe	Thr	Leu	Arq	Arq	Asp	Ala	Ser	Asn	His	Lys	Arq	Arg	Glu
2494		•	1719					172					172			
2495																
2496	Pro	Val	Gly	Gln	Asp	Ala	Val	Gly	Leu	Lys	Asn	Leu	Ser	Val	Gln	Val
2497		1730			-		1739	_		-		1740				
2498																
2499	Ser	Glu	Ala	Asn	Leu	Ile	${\tt Gly}$	Thr	Gly	Thr	Ser	Glu	His	${\tt Trp}$	Val	Asp

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2500 2501	174	5				1750	0				175	5				1760
2502 2503 2504	Asp	Glu	Gly	Pro	Gļn 176!		Lys	Lys	Val	Lys 177		Glu	Asp	Glu	Ala 1779	
2504 2505 2506 2507	Leu	Ser	Glu	Glu 1780	_	Asp	Pro	Ile	Asp 178!	_	Arg	Pro	Trp	Thr 1790		Gln
2508 2509 2510	His	Leu	Glu 179		Ala	Asp	Ile	Arg 1800	_	Thr	Pro	Ser	Leu 180!		Leu	Thr
2511 2512 2513	Pro	Pro 1810		Ala	Glu	Gln	Glu 181		Asp	Val	Leu	Asp 1820		Asn	Val	Arg
2514 2515 2516	Gly 182	Pro 5	Asp	Gly	Cys	Thr 1830		Leu	Met	Leu	Ala 183		Leu	Arg	Gly	Gly 1840
2517 2518 2519	Ser	Ser	Asp	Leu	Ser 184	_	Glu	Asp	Glu	Asp 185		Glu	Asp	Ser	Ser 185	
2520 2521 2522	Asn	Ile	Ile	Thr 1860	_	Leu	Val	Tyr	Gln 186	_	Ala	Ser	Leu	Gln 1870		Gln
2523 2524 2525	Thr	Asp	Arg 187		Gly	Glu	Met	Ala 1880		His	Leu	Ala	Ala 188	_	Tyr	Ser
2526 2527 2528	Arg	Ala 1890	_	Ala	Ala	Lys	Arg 189		Leu	Asp	Ala	Gly 1900		Asp	Ala	Asn
2529 2530 2531	Ala 190!	Gln 5	Asp	Asn	Met	Gly 1910	_	Cys	Pro	Leu	His 191		Ala	Val	Ala	Ala 1920
2532 2533	Asp	Ala	Gln	Gly	Val 192		Gln	Ile	Leu	Ile 1930	_	Asn	Arg	Val	Thr 1935	_
2534 2535 2536	Leu	Asp	Ala	Arg 1940		Asn	Asp	Gly	Thr 194!		Pro	Leu	Ile	Leu 1950		Ala
2537 2538 2539	Arg	Leu	Ala 195		Glu	Gly	Met	Val 1960		Glu	Leu	Ile	Asn 196!		Gln	Ala
2540 2541 2542 2543	Asp	Val 1970		Ala	Val	Asp	Asp 1975		Gly	Lys	Ser	Ala 1980		His	Trp	Ala
2544 2545	Ala 198!	Ala 5	Val	Asn	Asn	Val 1990		Ala	Thr	Leu	Leu 199!		Leu	Lys	Asn	Gly 2000
2546 2547 2548	Ala	Asn	Arg	Asp	Met 200!		Asp	Asn	Lys	Glu 201		Thr	Pro	Leu	Phe 201	
2549 2550	Ala	Ala	Arg	Glu	Gly	Ser	Tyr	Glu	Ala	Ala	Lys	Ile	Leu	Leu	Asp	His

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2551				2020)				202	5				203	0	
2552				_	_							_				
2553	Phe	Ala		_	Asp	IIe	Thr	_		Met	Asp	Arg			Arg	Asp
2554			203	5				204	0				2049	5		
2555			_				1									
2556	Val		_	Asp	Arg	Met			Asp	Ile	Val	_		Leu	Asp	Glu
2557		205	0				205!	5				206	0			
2558																
2559	${ t Tyr}$	Asn	Val	Thr	Pro	Ser	Pro	Pro	Gly	Thr	Val	Leu	Thr	Ser	Ala	Leu
2560	206	5				2070)				207	5				2080
2561																
2562	ser	Pro	Val	Ile	Cys	Gly	Pro	Asn	Arg	Ser	Phe	Leu	Ser	Leu	Lys	His
2563					2085	5				209)				209	5
2564																
2565	Thr	Pro	Met	Gly	Lys	Lys	Ser	Arg	Arg	Pro	Ser	Ala	Lys	Ser	Thr	Met
2566				210)				210	5				2110	0	
2567																
2568	Pro	Thr	Ser	Leu	Pro	Asn	Leu	Ala	Lys	Glu	Ala	Lys	Asp	Ala	Lys	Gly
2569			211!	5				212	ס _			_	212	5	_	_
2570																
2571	Ser	Arq	Arq	Lys	Lys	Ser	Leu	Ser	Glu	Lys	Val	Gln	Leu	Ser	Glu	Ser
2572		2130	_	•	•		213			•		214				
2573																
2574	Ser	Val	Thr	Leu	Ser	Pro	Val	Asp	Ser	Leu	Glu	Ser	Pro	His	Thr	Tvr
2575	214					2150					215					2160
2576		-					-					_				
2577	Val	Ser	Asp	Thr	Thr	Ser	Ser	Pro	Met	Tle	Thr	Ser	Pro	Glv	Ile	Leu
2578					2169		501			2170				011	2175	
2579					210.	•				/					/-	•
2580	Gln	Δla	Ser	Pro	Δgn	Pro	Met	Len	Δla	Thr	Δla	Δla	Pro	Pro	Ala	Pro
2581	0111	2114	501	2180				LCu	218		71 <u>1</u> u	7114	110	2190		110
2582										•						
2583	Val	His	Δla	Gln	Hig	Δla	T.e.11	Ser	Dhe	Ser	Δgn	T.e.11	Hig	Glu	Met	Gln
2584	• • • •		219				Lou	2200		501	11011	Lou	220			0211
2585														•		
2586	Pro	Leu	Δla	His	Glv	Δla	Ser	Thr	Val	Len	Pro	Ser	Val	Ser	Gln	Len
2587	110	2210			017	1114	2215		• • • •	a		2220		001	0111	Lou
2588		221	•				221.	•				222				
2589	T.011	Sar	ніс	ніс	Hie	Tla	Tal.	Ser	Pro	Glv	Sar	Glv	Sar	Δla	Gly	Sar
2590	222!		1113	1115	111.5	2230		SCI	FIO	Gry	223!	_	DCI	лта	Gry	2240
2591	222.	,				225	,				225.	,				2240
2592	T 011	Sor	7~~	T 011	uic	Dro	Val	Dro	1701	Dro	715	7 cm	Trn	Mot	Asn	71 200
2593	ьси	SET	Ar 9	ьeu	2245		vaı	F10	vaı	225		Tob	115	1.100	2255	_
2594					224.	,				225	,				223.	,
2595	Met	<u>@1.,</u>	Val	Δαν	Gl 11	Thr	Cl n	Ψιν	Δαν	ر1،	Met	Dhe	ر1 ، ر	Met	Val	T.611
2596	MEC	GIU	val	2260		TIIL	GIII	TÄT	226		rie C	FIIG	GTÅ	227		шeц
				2200	,				220	ر				22/	,	
2597 2598	7/1 ~	D~~	7/1 ~	C1	C1	Th∽	ui-	Dro	C1. -	T1.	7.1.	D~~	@1 ~	C~~	71 **~	Dro
	ATA	Pro			стλ	1111	uis		_	тте	ALG	PLO			Arg	PLO
2599			227	9				2280	J				2285)		
2600	Dwa	C1	~1	T	ui ~	T1 ~	ሞኮ ~	ሞ⊳∽	D~~	71	C1	Dwa	T 011	Droc	Dro	Tla
2601	PLO	GIU	σтλ	гуя	uis	тте	IIII	inr	PLO	Arg	GIU	PLO	ьeu	PLO	Pro	тте

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2602			229)				229	5				230	0			
2603					_												
2604				Phe	Gln	Leu			Lys	Gly	Ser			${\tt Gln}$	Pro	Ala	Gly
2605		2305	5				2310)				2315	5				2320
2606		_		_		_		_									
2607		Ala	Pro	Gln	Pro			Thr	Cys	Pro			Val	Ala	Gly	Pro	
2608						2325	5				2330)				2335	5
2609		_			_			_				_	_	_			_
2610		Pro	Thr	Met	_		Ile	Pro	GIu			Arg	Leu	Pro		Val	Ala
2611					2340)				2345	5				2350)	
2612		5 1-		m1.				_	~ 7	~ 7	_	~ 3	~-7			~ 3	_,
2613		Pne	Pro			Met	Met	Pro			Asp	GIY	GIn	_		Gln	Thr
2614				2355)				2360)				2365	•		
2615		T1 -		D	7.7.	m	TT -	D	D1	B				~ 1	_	_	_
2616		ше			Ата	Tyr	HIS			Pro	Ата	ser		_	гла	Tyr	Pro
2617			2370	,				2375	>		•		2380	,			
2618		mla sa	Dece	Desc	0	<u>ما -</u>	774	C	m	77-	0	C	7	77-	7 J -	a1	7
2619 2620		2385		PLO	ser	GIII	2390		TÀL	Ата	ser	2395		AIA	Ата	Glu	_
2621		236.	,				233(,				2333	,				2400
2622		Thr	Dro	Sar	Hic	Sar	Glv	Hic	T.011	Gln.	Gl ₃₇	Gl 11	Hic	Pro	Тъгъ	Leu	Thr
2623		1111	FIO	DCI	1113	2405	_	1113	пец	GIII	2410		1112	FIO	тут	2415	
2624						210.	,				271	,				211.	,
2625		Pro	Ser	Pro	Glu	Ser	Pro	Asp	Gln	Trn	Ser	Ser	Ser	Ser	Pro	His	Ser
2626			501		2420			1100	· · · ·	2425		-	501	501	2430		501
2627																	,
2628		Ala	Ser	Asp	Trp	Ser	Asp	Val	Thr	Thr	Ser	Pro	Thr	Pro	Glv	Gly	Ala
2629				2435	_		_		2440					2445	_	1	
2630																	
2631		Gly	Gly	Gly	Gln	Arg	Gly	Pro	Gly	Thr	His	Met	Ser	Glu	Pro	Pro	His
2632		_	2450)		_	_	2455	5				2460)			
2633																	
2634		Asn	Asn	Met	Gln	Val	Tyr	Ala									
2635		2465	5				2470)									
2636																	
2637	(2)	INFO	TAMS:	ON I	FOR S	SEQ]	D NO	20:20	:								
2638																	
2639		(i)				ARAC'				_							
2640						: 255		_	acio	is							
2641						amino											
2642						EDNES		_	Le								
2643			(D)	TOI	-OTO	3Υ: ι	ınkno	own									
2644		(++)	MOT	י דינוטק	י מינות ק	י ישר		4.									
2645 2646		(ii)	MOTI	COLI	7 I.XI	-r: I	epti	ıae									
2647																	
2648																	
2649		(xi)	SECT	IENCI	a Des	SCB TI	ירד∩ו	J. SI	ZO TI	אר כ	.20.						
2650		(451)	טבענ	1				51	-v -1	,0	. 2 .						
2651		Met	Pro	Pro	Leu	Leu	Ala	Pro	Leu	Leu	Cvs	Leu	Ala	Leu	Leu	Pro	Ala
2652		1				5					10					15	

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2653																
2654	T.011	Δla	Δla	Δνα	G1 17	Dro	Λrα	Carc	Sar	Gln	Dro	Gl v	Gl 11	Thr	Cys	T 011
2655	пси	AIG	ALG	20	Оту	110	Arg	Cys	25	GIII	FIO	СТУ	GIU	30	Cys	Deu
2656				20					23					30		
2657	Δan	Glv	Glv	Lare	Cve	G111	Δla	λla	Λen	Gly	Thr	G1 11	Λla	Cvc	Val	Cva
2658	ASII	Gry	35	БУЗ	Cys	GIU	Ата	40	ASII	GLY	1111	Gru	45	Cys	Val	Cys
2659			33					40					43			
2660	G1	C1	ת ד'ת	Dho	1701	C1	Dro	7. ~~	C	C1 5	7	Dwo	7. ~ ~	Dwo	Cys	T
2661	Gry	50	мта	FIIC	vaı	Сту	55	Arg	Cys	GIII	Asp		ASII	PLO	Cys	ьеu
2662		50					22					60				
2663	Cor	The	Dwo	C	Trea	7.45	77.	~1	The	C	II a	3707	1707	7	7. ~~~	7\ >===
2664		TILL	PIO	Сув	цув		Ата	СТА	TIIL	Cys		Val	Val	Asp	Arg	
	65					70					75					80
2665	~ 1	77-7	77-	7		77-	~		~		-	a 1	-1	~	~1	
2666	GIY	val	Ата	Asp		Ата	Cys	Ser	Cys		ьeu	GTA	Pne	ser	Gly	Pro
2667					85					90					95	
2668	Ŧ	~	.	6 01						~		m1	.	_	~	_
2669	Leu	Cys	Leu		Pro	Leu	Asp	Asn		Cys	Leu	Thr	Asn		Cys	Arg
2670				100					105					110		
2671	_	~7	~ 7	1	_	_	_	_	_,	_	_,	~-	_	_	_	_
2672	Asn	GLY	_	Inr	Cys	Asp	Leu		Thr	Leu	Thr	GLu	_	Lys	Cys	Arg
2673			115					120					125			
2674	_	_	_		_	_		_	_			-	_			
2675	Cys		Pro	GLY	Trp	Ser	_	Lys	Ser	Cys	Gln		Ala	Asp	Pro	Cys
2676		130					135					140				
2677								_	_	_				_	_	_
2678		Ser	Asn	Pro	Cys		Asn	Gly	Gly	Gln	_	Leu	Pro	Phe	Glu	
2679	145					150					155					160
2680																
2681	Ser	Tyr	Ile	Cys		Cys	Pro	Pro	Ser	Phe	His	Gly	Pro	Thr	Cys	Arg
2682					165					170					175	
2683	_		_													
2684	Gln	Asp	Val		Glu	Cys	Gly	Gln	Lys	Pro	Arg	Leu	Cys	Arg	His	Gly
2685				180					185					190		
2686	_															
2687	Gly	Thr		His	Asn	Glu	Val		Ser	Tyr	Arg	Cys		Cys	Arg	Ala
2688			195					200					205			
2689																
2690	Thr		Thr	Gly	Pro	Asn	Cys	Glu	Arg	Pro	Tyr		Pro	Cys	Ser	Pro
2691		210					215					220				
2692																
2693	Ser	Pro	Cys	Gln	Asn	${ t Gly}$	${ t Gly}$	Thr	Cys	Arg	Pro	Thr	${ t Gly}$	Asp	Val	Thr
2694	225					230					235					240
2695																
2696	His	Glu	Cys	Ala	_	Leu	Pro	${ t Gly}$	Phe	Thr	Gly	Gln	Asn	Cys	Glu	Glu
2697					245					250					255	
2698																
2699	Asn	Ile	Asp	_	Cys	Pro	Gly	Asn		Cys	Lys	Asn	Gly	Gly	Ala	Cys
2700				260					265					270		
2701						_										
2702	Val	Asp	_	Val	Asn	Thr	Tyr		Cys	Pro	Cys	Pro		Glu	\mathtt{Trp}	Thr
2703			275					280					285			

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2704																
2705	Gly	Gln	Tyr	Cys	Thr	Glu	Asp	Val	Asp	Glu	Cvs	Gln	Leu	Met	Pro	Asn
2706	•	290	-	-			295		-		•	300				
2707																
2708	Ala	Cvs	Gln	Asn	Glv	Glv	Thr	Cvs	His	Asn	Thr	His	Glv	Glv	Tvr	Asn
2709	305	- 2			2	310		-2 -			315		1	1	-1-	320
2710																
2711	Cvs	Val	Cvs	Val	Δsn	Glv	Trn	Thr	Glv	Glu	Δen	Cve	Ser	Glu	Δen	Tle
2712	0,0		0,0		325	0-1			017	330	1101	Cyb	001	014	335	
2713					323					330					333	
2714	7 an	7. an	Carc	Ala	602	ת ד ת	ת ד ת	Crra	Dho	uic	C1.	ח ד ת	Thr	Crra	Wic	7.00
2715	Asp	Asp	Cys	340	361	AIA	AIA	Cys	345	нтэ	Gry	Ата	1111	350	nis	Asp
2715				340					343					350		
2716	7 ~~	1701	717	Cor	Dho	TT	C	~1 ,,	C++C	Dro	ui a	a1	7)	mb w	a1	T 011
	Arg	vai		Ser	Pne	IÀT	Cys		Cys	PLO	птв	GTA	_	IIIL	GTA	Lеu
2718			355					360					365			
2719	T	~	TT 2	T	7	7	7.7	~	-1 -	a	7	D	~	3	a 1	al. .
2720 .	Leu	_	HIS	Leu	Asn	Asp		Cys	тте	ser	Asn		Cys	Asn	GIu	GIĀ
2721		370					375					380				
2722	_	_	_	_			_	_								_
2723		Asn	Cys	Asp	Thr		Pro	Val	Asn	Gly	_	Ala	Ile	Cys	Thr	_
2724	385					390					395					400
2725																
2726	Pro	Ser	${ t Gly}$	Tyr	Thr	${ t Gly}$	Pro	Ala	Cys	Ser	Gln	Asp	Val	Asp	Glu	Cys
2727	•				405					410					415	
2728																
2729	Ser	Leu	Gly	Ala	Asn	Pro	Cys	Glu	His	Ala	Gly	Lys	Cys	Ile	Asn	Thr
2730				420					425					430		
2731																
2732	Leu	Gly	Ser	Phe	Glu	Cys	Gln	Cys	Leu	Gln	Gly	Tyr	Thr	Gly	Pro	Arg
2733		_	435			_		440			_	_	445	_		_
2734																
2735	Cys	Glu	Ile	Asp	Val	Asn	Glu	Cys	Val	Ser	Asn	Pro	Cys	Gln	Asn	Asp
2736	-	450		-			455	-				460	-			-
2737																
2738	Ala	Thr	Cvs	Leu	Asp	Gln	Ile	Glv	Glu	Phe	Gln	Cvs	Met	Cvs	Met	Pro
2739	465		- 4		_	470					475			_		480
2740																
2741	Glv	Tvr	Glu	Gly	Val	His	Cvs	Glu	Val	Asn	Thr	Asp	Glu	Cvs	Ala	Ser
2742	1	-1-		1	485		-1-			490		F		-1-	495	
2743																
2744	Ser	Pro	Cvs	Leu	His	Asn	Glv	Ara	Cvs	Len	Asn	Lvs	Tle	Asn	Glu	Phe
2745	501		CyD	500		11011	017		505		1101	270		510	O-u	
2746				500					303					310		
2747	Gln	Cve	در ای	Cys	Dro	Thr	Glv	Dhe	Thr	Glv	Hie	Len	Cve	Gln	ጥኒታዮ	Aen
2748	0111	Cys	515	Cys	FIU	1111	OT Y	520	1111	GIY	1112	_cu	525	GIII	- Y -	voh
2749			213					J20					ديد			
2750	Va l	7/ 02	G1.,	Cvc	Δ 1 ¬	go-	ሞኮኍ	Dro	Circ	Laze	7/ 02	G1.,	лΙэ	Laze	Cva	T.011
2751	val	530	GIU	Cys	лта	DET	535	FIO	Cys	пуз	POII	540	лια	пув	Cys	ьeu
2751		550					233					J-± U				
2753	λαν	G137	Dro	λαν	ጥ ኮ ∽	ጥኒ፣ው	ጥኮኍ	Circ	Va l	Ctra	Thν	G1,,	<u>@</u>] 17	ጥኒታው	ሞኮ∽	Glaz
2754	545	GTA	FIO	Asn	TIIT	550	TILL	Cys	val	Cys	555	GIU	GIY	TAT	TILL	560
21JI	743					220					زرر					200

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2755																
2756	Thr	His	Cvs	Glu	Val	Asp	Ile	Asp	Glu	Cvs	Asp	Pro	Asp	Pro	Cys	His
2757			-1 -		565					570					575	
2758															3.3	
2759	Tvr	Glv	Ser	Cvs	Lvs	Asp	Glv	Val	Δla	Thr	Phe	Thr	Cvs	Len	Cys	Ara
2760	- 1 -	0-1		580	-10	1101	0-1		585				CyD	590	Cyb	1129
2761				500					303					220		
2762	Dro	G] v	Тче	Thr	G] v	Wic.	uic	Cva	C111	Thr	7 an	Tlo	7 an	C1.,	Cys	Cor
2763	FIU	Gry	595	1111	GIY	1112	птэ	600	GIU	1111	ASII	116		GIU	Cys	ser
			595					600					605			
2764	0	~1 ~	D	G	7	T	7	~ 1	ml	G	~1	7	D			
2765	ser		Pro	Cys	Arg	Leu	_	GIY	Thr	Cys	GIN	_	Pro	Asp	Asn	Ата
2766		610					615					620				
2767	_	_	_	_,	_	_	_					_	_			
2768		Leu	Cys	Phe	Cys		Lys	GТУ	Thr	Thr	_	Pro	Asn	Cys	Glu	
2769	625					630					635					640
2770																
2771	Asn	Leu	Asp	Asp		Ala	Ser	Ser	Pro		Asp	Ser	Gly	Thr	Cys	Leu
2772					645					650					655	
2773																
2774	Asp	Lys	Ile	Asp	Gly	Tyr	Glu	Cys	Ala	Cys	Glu	Pro	Gly	Tyr	Thr	Gly
2775				660					665					670		
2776																
2777	Ser	Met	Cys	Asn	Ser	Asn	Ile	Asp	Glu	Cys	Ala	Gly	Asn	Pro	Cys	His
2778			675					680		•		•	685		•	
2779																
2780	Asn	Glv	Glv	Thr	Cvs	Glu	Asp	Glv	Tle	Asn	Glv	Phe	Thr	Cvs	Arg	Cvs
2781		690	1		-1-		695	0-1			U-1	700		0,72	5	07.5
2782		020					023					, , ,				
2783	Pro	Glu	Glv	Tur	Hig	Δen	Pro	Thr	Cve	T.e.11	Ser	Glu	Val	Δen	Glu	Cve
2784	705	014		- 7 -	1120	710	110		Cyb		715	014		11011	O_u	720
2785	, 05					, 10					, 13					720
2786	Λen	Sar	λen	Dro	Care	Va l	uic	Cl.	λla	Carc	λκα	7 00	cor	T.011	Asn	C111
2787	ASII	SCI	ASII	FIO	725	Val	1113	Gry	AIG	730	Arg	ASD	261	пеп	735	Gry
2788					125					730					133	
2789	Trees	T 110	Crra	7.00	Cira	7 00	Dwo	~1	П	C 0 **	~1	mb w	7	C	7	T10
2790	ıyı	цуѕ	Cys		Cys	ASP	PIO	GIY	_	ser	GIY	1111	ASII	_	Asp	TIE
				740					745					750		
2791	7	7	7	~ 1	G	~ 1	G	7	D	~	**- 7	3	~1	~1	m1	a
2792	ASII	ASII		GIU	Cys	GIU	ser		Pro	Cys	vaı	ASII	_	GIA	Thr	Cys
2793			755					760					765			
2794	_	_			_	7			_		_					_
2795	ьуs		Met	Thr	Ser	GIA		Val	Cys	Thr	Cys		GIu	GIA	Phe	Ser
2796		770					775					780				
2797					_	_		_		_		_				
2798		Pro	Asn	Cys	Gln		Asn	Ile	Asn	Glu		Ala	Ser	Asn	Pro	Cys
2799	785					790					795					800
2800																
2801	Leu	Asn	Lys	Gly	Thr	Cys	Ile	Asp	Asp	Val	Ala	Gly	Tyr	Lys	Cys	Asn
2802					805					810					815	
2803																
2804	Cys	Leu	Leu	Pro	Tyr	Thr	Gly	Ala	Thr	Cys	Glu	Val	Val	Leu	Ala	Pro
2805				820					825					830		

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2806																
2807	Cys	Ala	Pro	Ser	Pro	Cys	Arg	Asn	Gly	Gly	Glu	Cys	Arq	Gln	Ser	Glu
2808	_		835			_	_	840	_	_		_	845			
2809																
2810	Asp	Tyr	Glu	Ser	Phe	Ser	Cys	Val	Cys	Pro	Thr	Ala	Gly	Ala	Lys	Gly
2811		850					855		_			860	_		_	_
2812																
2813	Gln	Thr	Cys	Glu	Val	Asp	Ile	Asn	Glu	Cys	Val	Leu	Ser	Pro	Cvs	Arq
2814	865		•			870				•	875				•	880
2815																
2816	His	Gly	Ala	Ser	Cys	Gln	Asn	Thr	His	Gly	Gly	Tvr	Arq	Cys	His	Cvs
2817		•			885					890	-	•		-	895	-
2818																
2819	Gln	Ala	Glv	Tvr	Ser	Glv	Ara	Asn	Cvs	Glu	Thr	Asp	Ile	Asp	Asp	Cvs
2820			-	900		•	_		905					910		- 2
2821																
2822	Ara	Pro	Asn	Pro	Cvs	His	Asn	Glv	Glv	Ser	Cvs	Thr	Asp	Gly	Ile	Asn
2823	- 5		915		_1			920	2		- 2		925			
2824																
2825	Thr	Ala	Phe	Cvs	Asp	Cvs	Leu	Pro	Glv	Phe	Ara	Glv	Thr	Phe	Cvs	Glu
2826		930		- 1	L	- 1	935		1	-	3	940			-1-	
2827																
2828	Glu	Asp	Ile	Asn	Glu	Cvs	Ala	Ser	Asp	Pro	Cvs	Ara	Asn	Gly	Ala	Asn
2829	945					950			1-		955	3				960
2830																
2831	Cvs	Thr	Asp	Cvs	Val	Asp	Ser	Tvr	Thr	Cvs	Thr	Cvs	Pro	Ala	Glv	Phe
2832	0,70			0,0	965	1101		-1-		970		- 7.5	110	1124	975	1
2833					,,,,					3,0					,,,	
2834	Ser	Glv	Ile	His	Cvs	Glu	Asn	Asn	Thr	Pro	Asp	Cvs	Thr	Glu	Ser	Ser
2835		1		980	-1-				985			012		990		
2836				500					,,,,					,,,,		
2837	Cvs	Phe	Asn	Glv	Glv	Thr	Cvs	Va l	Asp	Glv	Tle	Asn	Ser	Phe	Thr	Cvs
2838	-1-		995	1	1		-1-	1000		1			100!			-1
2839			,,,,													
2840	Leu	Cvs	Pro	Pro	Glv	Phe	Thr	Glv	Ser	Tvr	Cvs	Gln	His	Val	Val	Asn
2841		1010			1		101	_		-1-	-1-	1020				
2842								-					-			
2843	Glu	Cvs	Asp	Ser	Ara	Pro	Cvs	Leu	Leu	Glv	Glv	Thr	Cvs	Gln	Asp	Glv
2844	102					1030				1	1035		- 2			1040
2845																
2846	Arq	Glv	Leu	His	Arq	Cvs	Thr	Cvs	Pro	Gln	Glv	Tvr	Thr	Gly	Pro	Asn
2847		-			1045			•		1050		-		-	1055	
2848																
2849	Cys	Gln	Asn	Leu	Val	His	Trp	Cys	Asp	Ser	Ser	Pro	Cys	Lys	Asn	Gly
2850	•			1060			-	4	106				4	1070		4
2851																
2852	Gly	Lys	Cys	Trp	Gln	Thr	His	Thr	Gln	Tyr	Arg	Cys	Glu	Cys	Pro	Ser
2853	-	4	107	_				1080		4		-	108	_		
2854																
2855	Gly	Trp	Thr	Gly	Leu	Tyr	Cys	Asp	Val	Pro	Ser	Val	Ser	Cys	Glu	Val
2856	•	109		•		-	109	_				110		-		

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Ala Ala Gln Arg Gln Gly Val Asp Val Ala Arg Leu Cys Gln His Gly 2859 1105 1110 11115 11120 1120 1120 1105 1105 1110 11115 11120 1120 1120 1105 1105 1105 11125 11130 1135	2857																
2859		Ala	Ala	Gln	Ara	Gln	Glv	Val	Asp	Val	Ala	Ara	Leu	Cvs	Gln	His	Glv
2860 2861 2862 2863 2864 2865 2866 2866 2866 2866 2866 2867 2867 2868 2867 2868 2868					5		_		-10 F			_		070	0		_
2861 2862 2862 2863 2864 2862 2866 2866 2866 2866 2866 2866								-									
2862 2863 3 1125 1130 1135 2864 2865 3 1140 1145 1140 1150 2865 2866 6 1140 1145 1145 1150 2866 2867 2868 2868 2868 2868 2868 2868		Glv	Leu	Cvs	Val	Asp	Ala	Glv	Asn	Thr	His	His	Cvs	Ara	Cvs	Gln	Ala
2863 2864 2865 2866 2866 2866 2866 2866 2866 2867 2867		1		- 2		_		1					-1-	3	-7-		
2864 Gly Tyr Thr Gly Ser Tyr Cys Glu Asp Leu Val Asp Glu Cys Ser Pro												•					
2865 2866 2867 2868 2868 2869 2870 2870 2871 2871 2873 2873 2874 2875 2876 2876 2877 2873 2874 2876 2876 2877 2878 2879 2870 2870 2871 2871 2871 2871 2871 2872 2873 2874 2875 2876 2876 2876 2876 2877 2878 2879 2870 2877 2878 2879 2870 2876 2876 2877 2878 2879 2870 2877 2878 2879 2870 2877 2878 2879 2870 2876 2876 2876 2876 2877 2878 2879 2877 2878 2879 2870 2877 2878 2879 2870 2877 2878 2879 2870 2871 2877 2878 2879 2870 2871 2877 2878 2879 2870 2871 2877 2878 2879 2870 2871 2872 2872 2873 2874 2875 2876 2876 2877 2878 2879 2877 2878 2879 2870 2881 2882 2881 2882 2881 2882 2882 288		Glv	Tvr	Thr	Glv	Ser	Tvr	Cvs	Glu	Asp	Leu	Val	Asp	Glu	Cvs	Ser	Pro
2866 2867 Ser Pro Cys Gln Asn Gly Ala Thr Cys Thr Asp Tyr Leu Gly Gly Tyr 1165 2869 2870 Ser Cys Lys Cys Val Ala Gly Tyr His Gly Val Asn Cys Ser Glu Glu 1170 1175 1180 2871 1170 1170 1175 1180 2872 2873 Ile Asp Glu Cys Leu Ser His Pro Cys Gln Asn Gly Gly Thr Cys Leu 2874 1185 1190 1195 1200 2875 2876 Asp Leu Pro Asn Thr Tyr Lys Cys Ser Cys Pro Arg Gly Thr Gln Gly 1205 1220 12215 2878 2879 Val His Cys Glu Ile Asn Val Asp Asp Cys Asn Pro Pro Val Asp Pro 1220 1220 1225 1225 2880 1220 1220 1225 1225 1230 2881 1235 1240 1245 2884 2885 Val Gly Gly Tyr Ser Cys Thr Cys Pro Pro Gly Phe Val Gly Glu Arg 1255 1260 2886 1250 1250 1255 1270 1275 1280 2887 2888 Cys Glu Gly Asp Val Asn Glu Cys Leu Ser Asn Pro Cys Asp Ala Arg 1265 1270 1285 1290 2891 Gly Thr Gln Asn Cys Val Gln Arg Val Asn Asp Phe His Cys Glu Cys 1289 Arg Ala Gly His Thr Gly Arg Arg Cys Glu Ser Val Ile Asn Gly Cys 1310 1310 2896 2897 Lys Gly Lys Pro Cys Lys Asn Gly Gly Thr Cys Ala Val Ala Ser Asn 1315 1320 1325 1325 1325 1326 2897 Lys Gly Lys Pro Cys Lys Asn Gly Gly Thr Cys Ala Val Ala Ser Asn 1315 1330 1330 1335 1350 1350 2900 Thr Ala Arg Gly Phe Ile Cys Lys Cys Pro Ala Gly Phe Glu Gly Ala 1330 1335 1350 1360 2905 Gly Gly Thr Cys Ile Ser Gly Pro Arg Ser Pro Thr Cys Leu Cys Leu Asn 1345 1350 1350 1355		0-1	-1-				- 7 -	Cyb				• • • • • • • • • • • • • • • • • • • •	nop.	o_u			110
Ser Pro Cys Gln Asn Gly Ala Thr Cys Thr Asp Tyr Leu Gly Gly Tyr 1165 1160 1160 1165											_						
2868 2869 2869 2869 2869 2869 2869 2860 2870 2871 2871 2871 2871 2871 2871 2872 2873 2873 2874 2874 2874 2874 2874 2874 2874 2874 2874 2874 2874 2875 2876		Ser	Pro	Cvs	Gln	Δsn	Glv	Δla	Thr	Cva	Thr	Δan	Tur	T.e.11	Glv	Glv	Туг
2869 2870 Ser Cys Lys Cys Val Ala Gly Tyr His Gly Val Asn Cys Ser Glu Glu 2871 1170 1175 1180 2872 2873 Ile Asp Glu Cys Leu Ser His Pro Cys Gln Asn Gly Gly Thr Cys Leu 2874 1185 1190 1195 1200 2875 2876 Asp Leu Pro Asn Thr Tyr Lys Cys Ser Cys Pro Arg Gly Thr Gln Gly 2877 2878 2879 Val His Cys Glu Ile Asn Val Asp Asp Cys Asn Pro Pro Val Asp Pro 2880 1220 1225 1230 2881 2882 Val Ser Arg Ser Pro Lys Cys Phe Asn Asn Gly Thr Cys Val Asp Gln 2883 1235 1240 1245 2884 2885 Val Gly Gly Tyr Ser Cys Thr Cys Pro Pro Gly Phe Val Gly Glu Arg 2886 1250 1250 1255 1260 2887 2888 Cys Glu Gly Asp Val Asn Glu Cys Leu Ser Asn Pro Cys Asp Ala Arg 2889 1265 1270 1275 1280 2890 2891 2892 1285 1280 1290 1295 2893 Arg Ala Gly His Thr Gly Arg Arg Cys Glu Ser Val Ile Asn Gly Cys 2895 1300 Thr Ala Arg Gly Phe Ile Cys Lys Cys Pro Ala Gly Phe Glu Gly Ala 2897 2900 Thr Ala Arg Gly Phe Ile Cys Lys Cys Pro Ala Gly Phe Glu Gly Ala 2901 1330 Thr Cys Glu Asn Asp Ala Arg Thr Cys Gly Ser Leu Arg Cys Leu Asn 2904 1345 1350 1355 1360 2905 Gly Gly Thr Cys Ile Ser Gly Pro Arg Ser Pro Thr Cys Leu Cys Leu Cys Leu 2904 1345 1350 1355 1360		501				11011	O-7	1114		_	1111	АБР	- 7 -		_	CLY	1 7 1
Ser Cys Lys Cys Val Ala Gly Tyr His Gly Val Asn Cys Ser Glu Glu 1170					•					,					•		
2871		Ser	Cve	Lvc	Cvc	Val	Δla	Glv	Tur	Hic	Glv	Val	Δen	Cve	Ser	Glu	Glu
2872 2873		DCI	_	_	Cys	Val	AIU	_	_	111.5	Gry	Val			DCI	GIU	GIU
The Asp Glu Cys Leu Ser His Pro Cys Gln Asn Gly Gly Thr Cys Leu 1185 1190 1195 1200 1207				•					,				110	•			
2874 2875 2876		т1 о	7 cm	C1.,	Crrc	T 011	cor	uic	Drec	Crea	Cln	7 an	C1	C1	The	Cira	T 033
2875 2876 2876 2877 2877 2878 2879 2879 2880 2870 2880 2881 2882 2881 2882 2882 2883 2884 2885 2885 2886 2986 2987 2888 Cys Glu Gly Asp Val Asn Glu Cys Leu Ser Asn Pro Cys Asp Ala Arg Asp 2886 2887 2888 2889 2889 2889 2889 2889 2889			_	GIU	Cys	ьец			PIO	Cys	GIII		_	Gry	1111	Cys	
2876		110:	,				113	,				119:)				1200
2877 2878 2879 Val His Cys Glu Ile Asn Val Asp Asp Cys Asn Pro Pro Val Asp Pro 2880		7. ~~	T 017	Dwo	7 ~~	The	П	T	C	Com	C	Dwo	7	a 1	mb so	<i>α</i> 1	C1
2878 2879 2879 2880 2880 2880 1220 1225 1230 2881 2882 2882 2883 2884 2885 2886 2886 2886 2886 2887 2888 2886 2986 2987 2888 2988 2989 2890 2891 2890 2891 2891 2892 2891 2892 2892 2893 2894 2895 2893 2894 2895 2894 2895 2895 2896 2897 2898 2899 2900 2897 2898 2898 2900 2897 2898 2899 2900 2897 2898 2899 2900 2891 2890 2890 2891 2896 2897 2898 2899 2900 2891 2896 2897 2898 2899 2900 2891 2896 2897 2898 2899 2900 2891 2896 2897 2898 2898 2899 2900 2891 2896 2897 2898 2898 2899 2900 2891 2896 2899 2900 2891 2896 2899 2900 2891 2896 2899 2900 2891 2896 2897 2898 2898 2900 2898 2899 2900 2891 2898 2899 2900 2891 2896 2897 2898 2898 2900 2898 2899 2900 2891 2898 2899 2900 2891 2898 2899 2900 2896 2890 2890 2890 2890 2890 2890 2890 2890		Asp	ьеu	PIO	ASII			цуѕ	Cys	ser	_		Arg	GIY	Int		_
Val His Cys Glu Ile Asn Val Asp Asp Cys Asn Pro Pro Val Asp Pro 2880 1220 1225 1230 1235 1240 1245						120:)				121	,				1213	•
2880 2881 2882 2882 2883 2884 2885 2884 2885 2886 2886 2887 2888 2988 2988 2988 2988 2988 2988		370 T	Uic	C	C1	T10	7 ~~	17a l	7 ~~	7 ~~	C	7 ~~	Dro	Dree	3707	7 ~~	Dwo
2881 2882		vaı	птъ	Cys			ASII	vaı	Asp	_	_	ASII	PIO	PIO		_	Pro
2882 Val Ser Arg Ser Pro Lys Cys Phe Asn Asn Gly Thr Cys Val Asp Gln 2883 1235 1240 1245 2884 1235 1240 1245 2885 Val Gly Gly Tyr Ser Cys Thr Cys Pro Pro Gly Phe Val Gly Glu Arg 1260 2886 1250 1255 1260 2887 1260 1255 1260 2888 Cys Glu Gly Asp Val Asn Glu Cys Leu Ser Asn Pro Cys Asp Ala Arg 1280 2899 1265 1270 1275 1280 2891 Gly Thr Gln Asn Cys Val Gln Arg Val Asn Asp Phe His Cys Glu Cys 1290 1295 2892 1285 1290 1295 1295 2893 . 1300 1305 1310 1310 2896 . 1300 1305 1310 1310 2897 Lys Gly Lys Pro Cys Lys Asn Gly Gly Thr Cys Ala Val Ala Ser Asn 1325 1325 2899 1315 1320 1325 1340 2900 Thr Ala Arg Gly Phe Ile Cys Lys Cys Pro Ala Gly Phe Glu Gly Ala 1340 2902 1330 1335 1340 2903 Thr Cys Glu Asn Asp Ala					122(,				122:	5				123	,	
2883 2884 2885 2886 2886 2886 2887 2888 2888 2988 2988 2098 2008 2890 2890		77-7	~	7	a	D	*	a	D1 -		7	~ 1	m1	a	**- 7		a 1
2885		vaı	ser	_		Pro	ьуs	Cys			Asn	GIY	Thr	-		Asp	GIn
2885 Val Gly Gly Tyr Ser Cys Thr Cys Pro Pro Gly Phe Val Gly Glu Arg 2886 1250 1255 1260 2887 1288 Cys Glu Gly Asp Val Asn Glu Cys Leu Ser Asn Pro Cys Asp Ala Arg 2898 Asp Ala Arg 2889 1265 1270 1275 1280 2890 1285 1275 1280 2891 Gly Thr Gln Asn Cys Val Gln Arg Val Asn Asp Phe His Cys Glu Cys 1295 2892 1285 1290 1295 2893 . 1300 1305 1310 2895 1300 1305 1310 2896 1300 1305 1310 2897 Lys Gly Lys Pro Cys Lys Asn Gly Gly Thr Cys Ala Val Ala Ser Asn 1325 2899 1315 1320 1325 2899 1330 1335 1340 2900 Thr Ala Arg Gly Phe Ile Cys Lys Cys Pro Ala Gly Phe Glu Gly Ala 1340 2902 1335 1340 2903 Thr Cys Glu Asn Asp Ala Arg Thr Cys Gly Ser Leu Arg Cys Leu Asn 2904 1345 1350 1355 1360 2905 1306 1355 1360				1235	•				124()				124	>		
2886		7	~1	~ 1	_	a .	~	1	_	_	_	a 1	-1	1	~ 1	~7	_
2888		vaı	_	_	Tyr	Ser	Cys		_	Pro	Pro	GIY			GIY	GIU	Arg
2888			1250)				125	•				1260)			
2889 2890 2891 Gly Thr Gln Asn Cys Val Gln Arg Val Asn Asp Phe His Cys Glu Cys 2892 2893 2894 Arg Ala Gly His Thr Gly Arg Arg Cys Glu Ser Val Ile Asn Gly Cys 2895 2896 2897 Lys Gly Lys Pro Cys Lys Asn Gly Gly Thr Cys Ala Val Ala Ser Asn 2898 2899 2900 Thr Ala Arg Gly Phe Ile Cys Lys Cys Pro Ala Gly Phe Glu Gly Ala 2901 2902 2903 Thr Cys Glu Asn Asp Ala Arg Thr Cys Gly Ser Leu Arg Cys Leu Asn 2904 1345 1350 1350 1355 1360 2905 2906 Gly Gly Thr Cys Ile Ser Gly Pro Arg Ser Pro Thr Cys Leu Cys Leu		_		~ 7	_		_	~ 7	_	_	_	_	_		_		_
2890 2891 Gly Thr Gln Asn Cys Val Gln Arg Val Asn Asp Phe His Cys Glu Cys 2892 1285 1290 1295 2893 . 2894 Arg Ala Gly His Thr Gly Arg Arg Cys Glu Ser Val Ile Asn Gly Cys 2895 1300 1305 1310 2896 2897 Lys Gly Lys Pro Cys Lys Asn Gly Gly Thr Cys Ala Val Ala Ser Asn 2898 1315 1320 1325 2899 2900 Thr Ala Arg Gly Phe Ile Cys Lys Cys Pro Ala Gly Phe Glu Gly Ala 2901 1330 1335 1340 2902 2903 Thr Cys Glu Asn Asp Ala Arg Thr Cys Gly Ser Leu Arg Cys Leu Asn 2904 1345 1350 1355 1360 2905 2906 Gly Gly Thr Cys Ile Ser Gly Pro Arg Ser Pro Thr Cys Leu Cys Leu		_		GIY	Asp	vaı			Cys	ьeu	ser			Cys	Asp	Ата	_
2891 Gly Thr Gln Asn Cys Val Gln Arg Val Asn Asp Phe His Cys Glu Cys 2892 1285 1290 1295 2893 . 2894 Arg Ala Gly His Thr Gly Arg Arg Cys Glu Ser Val Ile Asn Gly Cys 2895 1300 1305 1310 2896 2897 Lys Gly Lys Pro Cys Lys Asn Gly Gly Thr Cys Ala Val Ala Ser Asn 2898 1315 1320 1325 2899 2900 Thr Ala Arg Gly Phe Ile Cys Lys Cys Pro Ala Gly Phe Glu Gly Ala 2901 1330 1335 1340 2902 2903 Thr Cys Glu Asn Asp Ala Arg Thr Cys Gly Ser Leu Arg Cys Leu Asn 2904 1345 1350 1355 1360 2905 2906 Gly Gly Thr Cys Ile Ser Gly Pro Arg Ser Pro Thr Cys Leu Cys Leu		126	•				12/	,				12/	>				1280
2892		~ 7	1	~1	_	_		~1	_		_	_	-1	'	_	~ 7	~
2894 Arg Ala Gly His Thr Gly Arg Arg Cys Glu Ser Val Ile Asn Gly Cys 2895 1300 1305 1310 2896 2897 Lys Gly Lys Pro Cys Lys Asn Gly Gly Thr Cys Ala Val Ala Ser Asn 2898 1315 1320 1325 2899 2900 Thr Ala Arg Gly Phe Ile Cys Lys Cys Pro Ala Gly Phe Glu Gly Ala 2901 1330 1335 1340 2902 2903 Thr Cys Glu Asn Asp Ala Arg Thr Cys Gly Ser Leu Arg Cys Leu Asn 2904 1345 1350 1355 1360 2905 2906 Gly Gly Thr Cys Ile Ser Gly Pro Arg Ser Pro Thr Cys Leu Cys Leu		GIY	Thr	GIn	Asn	_		GIn	Arg	vaı		_	Phe	Hls	Cys		_
2894 Arg Ala Gly His Thr Gly Arg Arg Cys Glu Ser Val Ile Asn Gly Cys 2895 1300 1305 1310 2896 2897 Lys Gly Lys Pro Cys Lys Asn Gly Gly Thr Cys Ala Val Ala Ser Asn 2898 1315 1320 1325 2899 2900 Thr Ala Arg Gly Phe Ile Cys Lys Cys Pro Ala Gly Phe Glu Gly Ala 2901 1330 1335 1340 2902 2903 Thr Cys Glu Asn Asp Ala Arg Thr Cys Gly Ser Leu Arg Cys Leu Asn 2904 1345 1350 1355 1360 2905 2906 Gly Gly Thr Cys Ile Ser Gly Pro Arg Ser Pro Thr Cys Leu Cys Leu						1285	•				1290)				1295)
2895 2896 2897 Lys Gly Lys Pro Cys Lys Asn Gly Gly Thr Cys Ala Val Ala Ser Asn 2898 2899 2900 Thr Ala Arg Gly Phe Ile Cys Lys Cys Pro Ala Gly Phe Glu Gly Ala 2901 2902 2903 Thr Cys Glu Asn Asp Ala Arg Thr Cys Gly Ser Leu Arg Cys Leu Asn 2904 1345 1350 1355 1360 2905 2906 Gly Gly Thr Cys Ile Ser Gly Pro Arg Ser Pro Thr Cys Leu Cys Leu		_			•	_,		_	_	_		_			_	~ 7	_
2896 2897		Arg	Ala	GIŻ			GLY	Arg	Arg	_		ser	vaı	тте		_	Cys
Lys Gly Lys Pro Cys Lys Asn Gly Gly Thr Cys Ala Val Ala Ser Asn 2898 1315 1320 1325 2899 2900 Thr Ala Arg Gly Phe Ile Cys Lys Cys Pro Ala Gly Phe Glu Gly Ala 2901 1330 1335 1340 2902 2903 Thr Cys Glu Asn Asp Ala Arg Thr Cys Gly Ser Leu Arg Cys Leu Asn 2904 1345 1350 1355 1360 2905 2906 Gly Gly Thr Cys Ile Ser Gly Pro Arg Ser Pro Thr Cys Leu Cys Leu					1300)				130	5				1310)	
2898		_		_	_	_	_	_			_,	_				_	_
2899 2900 Thr Ala Arg Gly Phe Ile Cys Lys Cys Pro Ala Gly Phe Glu Gly Ala 2901 1330 1335 1340 2902 2903 Thr Cys Glu Asn Asp Ala Arg Thr Cys Gly Ser Leu Arg Cys Leu Asn 2904 1345 1350 1355 1360 2905 2906 Gly Gly Thr Cys Ile Ser Gly Pro Arg Ser Pro Thr Cys Leu Cys Leu		Lys	GIY			Cys	ьуs	Asn			Thr	Cys	Ala			Ser	Asn
2900 Thr Ala Arg Gly Phe Ile Cys Lys Cys Pro Ala Gly Phe Glu Gly Ala 2901 1330 1335 1340 2902 2903 Thr Cys Glu Asn Asp Ala Arg Thr Cys Gly Ser Leu Arg Cys Leu Asn 2904 1345 1350 1355 1360 2905 2906 Gly Gly Thr Cys Ile Ser Gly Pro Arg Ser Pro Thr Cys Leu Cys Leu				1315	•				1320)				132	•		
2901 1330 1335 1340 2902 2903 Thr Cys Glu Asn Asp Ala Arg Thr Cys Gly Ser Leu Arg Cys Leu Asn 2904 1345 1350 1355 1360 2905 2906 Gly Gly Thr Cys Ile Ser Gly Pro Arg Ser Pro Thr Cys Leu Cys Leu		_,		_		_,			_	_	_		7	_,			
2902 2903 Thr Cys Glu Asn Asp Ala Arg Thr Cys Gly Ser Leu Arg Cys Leu Asn 2904 1345 1350 1355 1360 2905 2906 Gly Gly Thr Cys Ile Ser Gly Pro Arg Ser Pro Thr Cys Leu Cys Leu		Thr		_	GLy	Phe	Ile	_	_	Cys	Pro	Ala	_		Glu	GLY	Ala
2903 Thr Cys Glu Asn Asp Ala Arg Thr Cys Gly Ser Leu Arg Cys Leu Asn 2904 1345 1350 1355 1360 2905 2906 Gly Gly Thr Cys Ile Ser Gly Pro Arg Ser Pro Thr Cys Leu Cys Leu			1330)				1335	•				1340	ט			
2904 1345 1350 1355 1360 2905 2906 Gly Gly Thr Cys Ile Ser Gly Pro Arg Ser Pro Thr Cys Leu Cys Leu			_	-	_	_		_		_			_	_	_	_	_
2905 2906 Gly Gly Thr Cys Ile Ser Gly Pro Arg Ser Pro Thr Cys Leu Cys Leu			_	Glu	Asn	Asp		_	Thr	Cys	GLy			Arg	Cys	Leu	
2906 Gly Gly Thr Cys Ile Ser Gly Pro Arg Ser Pro Thr Cys Leu Cys Leu		1345	•				1350)				135	5				1360
		~ 7	~ 7		_		_	~ 7	_	_	_	_	1	~	_	~	
2907 1365 1370 1375		GLy	GLY	Thr	Cys			GŢŻ	Pro	Arg			Thr	Cys	Leu		
	2907					T365	•				1370	J				T375	

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2908																
2909	Gly	Pro	Phe	Thr	Gly	Pro	Glu	Cys	Gln	Phe	Pro	Ala	Ser	Ser	Pro	Cys
2910	_			1380				•	138					139		•
2911																
2912	Leu	Gly	Gly	Asn	Pro	Cys	Tyr	Asn	Gln	Gly	Thr	Cys	Glu	Pro	Thr	Ser
2913		-	139			-	-	140		•		•	140			
2914																
2915	Glu	Ser	Pro	Phe	Tyr	Arq	Cvs	Leu	Cvs	Pro	Ala	Lvs	Phe	Asn	Glv	Leu
2916		1410			-	,	141		- 4			142			1	
2917												_				
2918	Leu	Cvs	His	Ile	Leu	Asp	Tvr	Ser	Phe	Glv	Glv	Glv	Ala	Glv	Ara	Asp
2919	1425					1430				1	143			1	3	1440
2920		-					=									
2921	Ile	Pro	Pro	Pro	Leu	Tle	Glu	Glu	Δla	Cvs	Glu	T.em	Pro	Glu	Cvs	Gln
2922					1445		<u></u>	014	1114	145		Lou		O_u	145	
2923						•					•					
2924	Glu	Asp	Δla	Gly	Δsn	Lvs	Val	Cvs	Ser	T.e.11	Gln	Cve	Δen	Δcn	Hic	Δla
2925	مدت	7101	1120	1460	-	,	Val	Cys	146		0111	Cys	ASII	1470		AIG
2926				1100	,				140.	_				14/	,	
2927	Cvs	Glv	Tro	Asp	Glv	Glv	Agn	Cve	Ser	T.e.11	Δen	Dhe	Δen	Δen	Dro	Trn
2928	Cyb	O _T y	1475	_	Gry	O _T y	тор	1480		пец	ASII	FIIC	148	_	FIO	пр
2929			14/.	_				140	,				140.	,		
2930	Lare	λen	Cvc	Thr	Gln	Sar	LOU	Cln.	Carc	Trn	Tarc	Тиг	Dho	602	7 02	C1.,
2931	цуз	1490	_	1111	GIII	561	1495		Cys	тър	цуз	1500		261	АБР	GIY
2932		1431	5				147.	,				1300	J			
2933	wic	Carc	7 cm	Ser	Gln	Cvc	7 an	cor	ת 1 ת	C111	Cura	T 011	Dho	7 02	C1.,	Dho
2934	1505		Asp	ser	GIII	151		ser	Ата	GTÀ	-		Pne	ASP	СТА	
2935	1505	,				TOT					1515	,				1520
2936	7 020	Crra	Cl n	7 ~~	70.7	C1	C1	۵1 ₅	C	7	Drea	T 011	TT	7	71 -	m
2937	ASP	Cys	GTII	Arg			СТУ	GIII	Cys			ьeu	Tyr	Asp		-
2938					1525	,				153	,				1535	•
2939	C	T	7	TT	Dho	C 0 20	7	a 1	TT	G	7	al =	a 1	G	7	0
2940	Cys	гуѕ	Asp	His		ser	Asp	GIY		_	Asp	GIII	GIY	_		ser
2941				1540	,				154)				1550	J	
2941	777	a1	Crra	<i>α</i> 1	Пип	7	a1	T 011	7	C	71.	a1	TT-1 -	7707	D	<i>α</i> 1
2943	Ala	GIU	1555	Glu	пр	Asp	СТУ		_	Cys	Ата	GIU			Pro	GIU
2944			155	•				1560	J				156	•		
	7. 20.00	т	77.	777	a 1	mb	T 0	77-7	77-7	17-1	77-7	T	1.6 a. b.	D	D	a 1
2945	_			Ala	GTA	Thr			vai	vai	vai			Pro	Pro	GIU
2946	′	1570	J				1575	•				1580	J			
2947	~ 1	7	7	7	0	0	Dl	TT-1	DI	.	3	~1	T	0	7	77- 7
2948			Arg	Asn	ser			HIS	Pne	Leu	_		ьeu	ser	Arg	
2949	1585	•				1590	,				1595	>				1600
2950	T	***	m1	3	77- 7	77-7	D1	.	7	3	3 7 -		~ 1	~ 1	~ 1	34 - 1
2951	ьeu	HIS	ınr	Asn			Pne	гда	Arg	_		H1S	GТĀ	GIN		
2952					1605	•				161	J				1615	
2953	71 .	DI	D	m	m	a 2	7	a 2 -	~ 1	~ 1	T	.	-	***	D-	- 1
2954	тте	Pue	Pro	Tyr	_	GTA	arg	GIU			ьеи	Arg	ьуs			тте
2955				1620	,				162	5				1630	J	
2956	T	7	7.7 -	7. T -	a 1	a 1	m	7 7 -	~ T -	ъ.	7 . ~		-	-	a ·	a 1.
2957	ьys	arg		Ala	GIU	стХ	ırp			Pro	ASP	ата			GTA	GIN
2958			1635)				1640	J				164	•		

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2959																
2960	Val	T.ve	Δla	Ser	T. - 11	T.011	Dro	Gl v	Gl ₃₇	Car	Glu	Gl ₃₇	G137	7 200	λνα	λνα
2961	val	1650		DCI	пси	шси	1659		Gry	JCI	Giu	1660	_	Arg	nr 9	nrg
2962		1050	•				100.	•				1000	,			
2963	Arg	Glu	T.e.11	Δen	Pro	Met	Agn	Va l	Δrα	Glv	Ser	Tle	Va 1	Туг	T.011	Glu
2964	1665		cu	тор	110	1670		val	A. 9	Ory	1675		val	T Y L	пси	1680
2965	1005	'				1070	,				107.	,				1000
2966	т1Д	λen	λen	λνα	Gln	Cvc	1721	Gln	λla	Sar	Sar	Gln	Cvc	Dhe	Gln	Car
2967	110	пор	ASII	n. g	1685	-	var	0111	AIG	1690		0111	Cys	FIIC	1695	
2968					100.	,				1030	,				109.	,
2969	Ala	Thr	λen	T/al	Λla	λla	Dha	T.Au	Gl v	Nlα	Lau	ת [ת	Car	T 011	C137	Sor
2970	AIG	- 111	пор	1700		AIG	riic	пси	1705		пси	AIG	561	1710	-	Ser
2971				1,00	•				170.	,				1/10	,	
2972	Leu	λen	Tla	Dro	Тугт	T.sze	Tla	Glu.	Nlα	Wal	Gln	Car	Glu.	Thr	Va l	Clu
2973	пси	ASII	1719		TYT	цуз	110	1720		vai	GIII	DCI	1729		vai	Giu
2974			1/1.	,				1/20	,				1/2.	,		
2975	Pro	Dro	Dro	Dro	777	Cln	T 011	Wi c	Dho	Mot	Ттг	7727	71-	71-	ת דת	ח ד ת
2976	PIO	1730		FIO	Ата	GIII	1735		PILE	MEC	тут	1740		Ala	Ата	AIA
2977		1/30	,				1/3	,				1/40	,			
2978	Phe	Val.	T 011	Teu	Dhe	Dho	Val.	Clv	Cva	C117	Wal	T 011	T 011	Cor	71 200	Two
2979	1745		пец	пец	FILE	1750		GTY	Cys	GTY	1755		пеп	261	Arg	1760
2980	1/43	1				1/50	,				1/5)				1/60
2981	7 200	7 ~~~	7 ~~~	C1 -	uia	~1	C1 ~	T 011	Two	Dho	Dwo	C1	C1	Dho	T	3707
2982	Arg	Arg	Arg	GIII	1765	_	GIII	ьeu	пр			GIU	СТУ	Pne		
2983					1/6:	,				1770	,				1775	•
2984	Com	~1	77.	Com	T	T	T	7 200	7. 200	α1	<u>ما</u>	T	~1	<u>ما</u>	7. ~~~	C
	Ser	GIU	Ата			гуѕ	гуѕ	Arg			GIU	ьeu	СТА			ser
2985				1780	,				1789	•				1790	J	
2986	7707	~1··	T	T	Desc	T	T	7	77-	C	7 ~~	a1	77-	T	N/ - +	7 ~~~
2987 2988	Val	GIÀ	1799		Pro	Leu	гуѕ	1800		ser	Asp	GIA			мес	Asp
2989			1/95	•				1000	,				1805	,		
2989	Asp	7 02	C1 5	7 00	~1.,	Two	C1	Nan	C1	Nan	T 011	C1	The	Tara	Tira	Dho
2991	Asp	1810		ASII	GIU	тъ	1815		GIU	Asp		1820		цуѕ	ьуя	Pne
2992		1010	,				101:	,				1020	,			
2993	7\ >=<	Dho	~1	~1	Dwo	W-1	17.01	T 011	Dwo	7 ~~	T 011	7 ~~	7 ~~	C1-	mb w	70.000
2994	Arg 1825		GIU	GIU	PIO	1830		ьец	PIO	Asp	1835	_	Asp	GIII	THE	1840
2995	1023					103	,				103	,				1040
2996	His	Λνα	Gln.	Trn	Thr	Cln	Gln.	Wi c	Tou	λan	712	712	7 an	Tou	7/200	Mot
2997	1115	Arg	GIII	тъ	1845		GIII	nis	пеп	1850		Ата	Asp	пеп	1855	
2998					1045	,				103(,				1000	,
2999	Sor	712	Mo+	712	Dro	Thr	Dro	Dro	Cln	C111	C111	17-1	7 000	71.	Asp	Cara
	Ser	Ата	Mec			TIII	PIO	PIO			GIU	val	Asp			Cys
3000 3001				1860	,				1869	,				1870	,	
3002	Met	7 an	va 1	7 cn	Wa I	7/200	C117	Dro	7 an	C1	Dho	Thr	Dxo	T 011	Mot	Tlo
3002	MEC	wsb	1875		val	ALG	GTA	1880	_	ату	FIIE	TIIT.			MEL	TTG
3003			10/5	,				T00(,				1889	,		
3004	Ala	Co~	Carc	Se.~	G1.,	Cl.	C1	T 033	C1	Th∽	G1	7 ~~	C0~	C1	C1	C1
3005	AId		_	261	GTÀ	ату	1895		GIU	111L	GTÀ			GIU	GIU	GIU
3006		1890	,				1033	,				1900	,			
3007	Glu	Aen	Δla	Dro	Δla	V=1	Tle	Ser	λαν	Dhe	Tle	ጥረታው	Gla	G1.77	712	Sa~
3009	1905		nia	FIO	nia	1910		SET	чэр	FIIG	1919		9111	GIY	нта	1920
5009	1903	,				エクエし	,				121	,				1920

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2010																
3010 3011	т	TT-1	7	a1	m1	7	7	m1	~1	a 1	m1	77-	T	TT 2 -	.	n 1 -
3011	Leu	HIS	ASII	GIII	192		Arg	Thr	GIY			Ala	ьeu	His		
					192:	•				1930	J				193	•
3013	ח ד ת	71	TT	Com	7	C 0	7	77.	77.	T	7	т	T 0	a 1	77.	C
3014	Ата	Arg	Tyr			ser	Asp	Ата			Arg	Leu	Leu	Glu		ser
3015				1940	,				194	5				1950	J	
3016		_		_	- 1	~1	_	_		~-7	_		_	_	•	
3017	Ala	Asp			тте	GIN	Asp			GIY	Arg	Thr		Leu	HIS	Ата
3018			195!	>				196	Ü				196	5		
3019			_		_		~ 7	~-7		_,	~-7		_		_	_
3020	Ата			Ата	Asp	Ата		_	vaı	Pne	GIn			Ile	Arg	Asn
3021		1970	J				197	•				1980	U			
3022	_		_,	_	_	_		_			_				_	_
3023	_		Thr	Asp	Leu	_		Arg	Met	His	-	_	Thr	Thr	Pro	
3024	1985	5				1990)				1999	5				2000
3025		_			_	_						_		_		
3026	Ile	Leu	Ala	Ala	_		Ala	Val	Glu	_		Leu	Glu	Asp		
3027					2009	5				2010)				201	5
3028				_		_		_	_							_
3029	Asn	Ser	His		_	Val	Asn	Ala		_	Asp	Leu	Gly	Lys		Ala
3030				2020)				202	5				2030)	
3031																
3032	Leu	His	-		Ala	Ala	Val			Val	Asp	Ala		Val	Val	Leu
3033			203	5				204	0				204	5		
3034																
3035	Leu			${ t Gly}$	Ala	Asn			Met	Gln	Asn			Glu	Glu	Thr
3036		2050)				205	5				206	0			
3037																
3038			Phe	Leu	Ala		_	Glu	Gly	Ser	Tyr	Glu	Thr	Ala	Lys	Val
3039	206	5				2070)				2075	5				2080
3040																
3041	Leu	Leu	Asp	His	Phe	Ala	Asn	Arg	Asp	Ile	Thr	Asp	His	Met	Asp	Arg
3042					2085	5				2090)				2095	5
3043																
3044	Leu	Pro	Arg	Asp	Ile	Ala	Gln	Glu	Arg	Met	His	His	Asp	Ile	Val	Arg
3045				2100)				210	5				2110)	
3046																
3047	Leu	Leu	_		Tyr	Asn	Leu	Val	Arg	Ser	Pro	Gln	Leu	His	Gly	Ala
3048			211	5				2120)				212	5		
3049																
3050	Pro	Leu	Gly	Gly	Thr	Pro	Thr	Leu	Ser	Pro	Pro	Leu	Cys	Ser	Pro	Asn
3051		2130)				213	5				214	0			
3052																
3053	_	_	Leu	Gly	Ser		_	Pro	Gly	Val		_	Lys	Lys	Val	_
3054	214	5				2150	כ				2155	5				2160
3055																
3056	Lys	Pro	Ser	Ser			Leu	Ala	Cys			Lys	Glu	Ala		
3057					2165	5				2170)				2175	5
3058																
3059	Leu	Lys	Ala	_	_	Lys	Lys	Ser		_	Gly	Lys	Gly	Cys		Leu
3060				2180)				218	5				2190)	

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3061																
3062	Δsn	Ser	Ser	Glv	Met	T.611	Ser	Dro	Val	Δen	Sar	Lau	Glu	Car	Dro	Wic.
3063	тър	DCI	219		1100	Lcu	DCI	2200		App	DCI	пец	220!		PIO	1115
3064								220	,				220.	,		
3065	Glv	Tyr	T.e.ii	Ser	Δsn	Val	Δla	Ser	Dro	Dro	T.011	T.011	Pro	Sar	Dro	Dhe
3066	017	221		501	nsp	VUI	221		110	110	пси	2220		Ser	FIO	FIIC
3067		221	,				221.	,				222(,			
3068	Gln	Gln	Ser	Pro	Ser	Val	Dro	T.011	Δen	Hic	T.011	Dro	Glv	Mot	Dro	Λαn
3069	222		DCI	110	261	2230		пец	ASII	1113	223		GIY	MEC	PIO	2240
3070	222	,				223	,				443.	,				2240
3071	Thr	His	Lou	Glaz	T10	Clv	uic	Lou	7 cn	17a l	717	אן ה	Tara	Dro	c1,,	Mot
3072	1111	1115	шец	GTY	2245		птъ	Бец	ASII	2250		Ата	цур	PIO	2255	
3072					224.	,				223	,				225	,
3074	ת דת	Ala	Lou	Glar	G117	C111	C111	7~~	T 011	ת דת	Dho	C1,,	mb~	C1	Dwo	Dwo
3075	AIG	AIG	пец	2260	_	GIY	СТУ	Arg	2265		FILE	GIU	1111	-		PIO
3075				2200	,				2203	,				2270	,	
3077	7 ra	Leu	cor	шic	Lou	Dro	7727	71-	cor	C111	Thr	Cor	Thr	170 T	T 011	C1
3078	Arg	пец	227		пец	PIO	val	2280		GIY	1111	Ser	228		цец	GIY
3078			227.	,				2200	,				220	,		
3080	Car	Ser	Cor	Glw	Glv	בות	Lau	Λαn	Dho	Thr	772 J	C111	C1,,	cor	Thr	Cor
3081	Ser	2290		GTA	GTA	Ата	229		PILE	TILL	val	2300	_	ser	IIII	ser
3082		223	,				223					2300	,			
3082	Lau	Asn	Glaz	Gln	Cvc	C111	Trn	T 011	cor	7 ~~	T 011	Cln	cor	C111	Mo+	val.
3084	230		СТУ	GIII	Cys	2310	_	Leu	ser	Arg			ser	GIY	Met	
3085	230.	5				2310	,				2319	,				2320
3086	Dro	7.00	~1 _n	Тист	7 ~~	Dro	T 011	7 ~~~	C1	Cox	770.1	77-	Dwa	<i>α</i> 1	Dwo	T 011
3087	PIO	Asn	GIII	TAT	2325		ьец	Arg	GTA			Ala	PIO	GIY		
3088					232.	,				2330	,				2335	,
3089	cor	Thr	Cl n	712	Dro	Car	Lou	Gl n	uic	C137	Mot	1721	C111	Dro	T 011	ui c
3090	261	1111	GIII	2340		261	пец	GIII	2345	_	Mec	vai	Gry	2350		пть
3091				2340	,				2343	,				2350	,	
3092	Sor	Ser	T 011	712	712	cor	ת ד ת	T 011	cor	Cln	Mo+	Mo+	602	Tare	Cln	C1.,
3093	261	261	235		Ата	261	Ата	2360		GIII	1.100	Mec	2365		GIII	Giy
3094			233.	,				2300	,				230.	,		
3095	I.ėu	Pro	Sar	Thr	Δνα	Τ.Δ11	Δla	Thr	Gln	Dro	Hie	T.011	Val.	Gln	Thr	Gln
3096	ЦСЦ	2370		1111	AI 9	пси	2375		GIII	FIO	111.5	2380		GIII	1111	GIII
3097		237	•				2375	•				2300	•			
3098	Gln	Val	Gln	Pro	Gln	Δen	T.e.11	Gln	Mot	Gln	Gln	Gln	Δen	T.011	Gln	Dro
3099	238		0111		0111	2390		0111		0111	239		11011	_cu	0111	2400
3100	230	_				2330	•				200.					2100
3101	Ala	Asn	Tle	Gln	Gln	Gln	Gln	Ser	Len	Gln	Pro	Pro	Pro	Pro	Pro	Pro
3102					2405					2410					2415	
3103											•					-
3104	Gln	Pro	His	Leu	Glv	Val	Ser	Ser	Δla	Ala	Ser	Glv	His	Leu	Glv	Ara
3105				2420					2425			1		2430	_	5
3106				`						-						
3107	Ser	Phe	Leu	Ser	Glv	Glu	Pro	Ser	Gln	Ala	Asp	Val	Gln	Pro	Leu	Glv
3108			243		1			2440			E		2445			1
3109				_				'	_					-		
3110	Pro	Ser	Ser	Leu	Ala	Val	His	Thr	Ile	Leu	Pro	Gln	Glu	Ser	Pro	Ala
3111		2450					245					2460				
												•				

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3112																		
3113	,	Leu	Pro	Thr	Ser	Leu	Pro	Ser	Ser	Leu	ı Val	Pro	Pro	Val	Thr	Ala	Ala	
3114		246	5				247	0				247	5				2480	
3115																		
3116		Gln	Phe	Let	ı Thr	Pro	Pro	Ser	Ģln	His	ser	Tyr	Ser	Ser	Pro	Val	Glu	
3117						248	5				249	0				249	5	
3118																		
3119		Asn	Thr	Pro	Ser	His	Gln	Leu	Gln	Val	. Pro	Glu	His	Pro	Phe	Leu	Thr	
3120					250	0				250	5				251	.0		
3121																		
3122		Pro	Ser	Pro	Glu	Ser	Pro	Asp	Gln	Trp	Ser	Ser	Ser	Ser	Pro	His	Ser	
3123				251				_	252					252				
3124																		
3125		Asn	Val	Ser	gaA :	Trp	Ser	Glu	Gly	Val	. Ser	Ser	Pro	Pro	Thr	Ser	Met	
3126			253		-	_		253					254					
3127																		
3128		Gln	Ser	Glr	ılle	Ala	Ara	Ile	Pro	Glu	ı Ala	Phe	Lvs					
3129		254					255					255	_					
3130													_					
3131	(2) I	NFO	RMAT	'ION	FOR :	SEO	ID N	0:21	:									
3132	, _ ,	_				~												
3133		(i)	SEC	UENC	E CH	ARAC'	TERT	STIC	S:									
3134		,			ENGTH					s								
3135					PE: 1					~								
3136					RAND				ا و									
3137			• -		POLO													
3138			(1)	,	71010	.	WIII	O										
3139	1	ii)	MOT	ECIII	E TY	DE.	срид											
3140	,	,					021171											
3141																		
3142	(ix)	FEA	TURE	2 •													
3143	`	 ,			ME/K	rv.	CDS											
3144					CATI			7419										
3145			(1	, 110	CAII	O14 .	10	/41)										
3146																		
3147	1	vi)	SEC	TENC	E DE	C C D T	ייים	M C	г∩ т	ם אור	1.21.							
3148	ν.	X 1 /	OLQ	CLIVE	ים בי	OCKI	FILO	N. D.	ב עם	D NC	,.ZI.							
3149	GGAAT'	ጥሮር	מ ככ	יר פר	יר כידי	ם רם	ת תת	ר מרי	т ст	ים ריז	ים דם	ים פרי	<u>а</u> Ст/	<u>ч</u> Ст.	מ מר	ים	41	Ω
3150	GGAAI	100			a Le													0
3151				1	a ne	u AI	_	5	а пс	u ne	u	P A10		и пе	u AI	.a		
3151				_				_				Τ,	•					
3152	CTC T	CC.	CTC	TCC	TCC	ccc	aaa .	aaa .	200	מאידי	CCA	TTC (מאמי	ror .	CCA	CAT	9(c
3153	CTC To																91	J
		_	ьец	Cys	Cys .	нта.		PIO.	нта	птъ	АТА		GIII '	cys .	Arg	Asp		
3155		15					20					25						
3156 3157	GGC T.	יתי א	~ 7 7	ccc	TOTAL A	עידים	ייית ע	ር አ አ	3 C27	አጥሮ	тСт	<u>с</u> ттт .	אממי	דאר י	מאמ	א א ידי	14.	1
3157																	14	4
3158	Gly T	λr	GIU	PLO	сув		ASII (GIU	атХ	MEL	_	val	TIIL	TAT.	птВ			
3159 3160	30					35					40	•				45		
2700																		
	CCC A	C۷	CC3	ጥልረ	TCC	<u>አ</u> አአ	ጥረም ፡	ממא .	ת תיבי	aaa	ттс	т тт	ggg ,	ግ አ አ	ጥለጥ	тст	1 0	2
3161 3162	GGC A																19:	2

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3163					50					55					60		
3164 3165	CAA	CAT	CGA	GAC	CCC	TGT	GAG	AAG	AAC	CGC	TGC	CAG	AAT	GGT	GGG	ACT	240
3166	_	His															
3167				65					70					75			
3168 3169	тст	GTG	CCC	CAG	CCC	λπα	СТС	ccc	71 71 71	ccc	NCC.	TCC	CCA	TOT	ccc	TIC N	288
3170		Val															200
3171	-1-		80					85				0,70	90	0,70		-	
3172																	
3173		TTT															336
3174	Gly	Phe	Thr	Gly	Glu	Asp	_	Gln	Tyr	Ser	Thr		His	Pro	Cys	Phe	
3175 3176		95					100					105					
3177	GTG	тст	CGA	CCC	TGC	CTG	ААТ	GGC	GGC	ACA	TGC	CAT	ATG	CTC	AGC	CGG	384
3178		Ser															
3179	110		_		-	115		_	_		120					125	
3180																	
3181		ACC															432
3182	Asp	Thr	Tyr	Glu	_	Thr	Cys	GIn	Val	_	Phe	Thr	GГĀ	Lys		Cys	
3183 3184					130					135					140		
3185	CAA	TGG	ACG	GAT	GCC	TGC	СТС	тст	САТ	CCC	тст	GCA	ААТ	GGA	AGT	ACC	480
3186		Trp															100
3187		-		145		•			150		4			155			
3188																	
3189		ACC															528
3190	Cys	Thr		Val	Ala	Asn	Gln		Ser	Cys	Lys	Cys		Thr	Gly	Phe	
3191 3192			160					165					170				
3193	ACA	GGG	CAG	AAA	тст	GAG	ACT	GAT	GTC	ААТ	GAG	тст	GAC	АТТ	CCA	GGA	576
3194		Gly															•
3195		175		•	-		180	_				185	_			-	
3196																	
3197		TGC															624
3198		Cys	GIn	Hls	GLY	195	Thr	Cys	Leu	Asn		Pro	GIY	ser	Tyr		•
3199 3200	190					193					200					205	
3201	TGC	CAG	TGC	CCT	CAG	GGC	TTC	ACA	GGC	CAG	TAC	TGT	GAC	AGC	CTG	TAT	672
3202		Gln															
3203					210					215					220		
3204																	
3205		CCC															720
3206 3207	vaı	Pro	Cys	A1a 225	Pro	ser	Pro	cys	230	ASI	GTÅ	сту	ınr	235	Arg	GIII	
3207				رےے					230					200			
3209	ACT	GGT	GAC	TTC	ACT	TTT	GAG	TGC	AAC	TGC	CTT	CCA	GGT	TTT	GAA	GGG	768
3210	Thr	Gly	Asp	Phe	Thr	Phe	Glu		Asn	Cys	Leu	Pro	Gly	Phe	Glu	Gly	
3211			240					245					250				
3212	7.00	700	mam	az	7.00	יחיקע	7 100	CI TO THE	07 C	maa	COM	7 7 C	CT C	700	mam	C 7 C	016
3213	AGC	ACC	TGT	GAG	AGG	AAT'	ATT	GAT	GAC	TGC	CCT	AAC	CAC	AGG	TGT	CAG	816

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3214 3215 3216	Ser	Thr 255	Cys	Glu	Arg	Asn	Ile 260	Asp	Asp	Cys	Pro	Asn 265	His	Arg	Cys	Gln	
3217 3218 3219 3220				GTT Val													864
3221 3222 3223 3224				TGG Trp													912
3225 3226 3227 3228				CCC Pro 305													960
3229 3230 3231 3232				TAT Tyr													1008
3233 3234 3235 3236				AAC Asn													1056
3237 3238 3239 3240				ATC Ile													1104
3241 3242 3243 3244				GGT Gly													1152
3245 3246 3247 3248				AAG Lys 385													1200
3249 3250 3251 3252				ACC Thr													1248
3253 3254 3255 3256				GAA Glu													1296
3257 3258 3259 3260				GTG Val													1344
3261 3262 3263 3264				GGA Gly													1392

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3265 3266				CAG Gln													1440
3267 3268	P	110	0,70	465	11011	пор	1124		470	Lea	пор	2,5	110	475	Cly	1110	
3269				TGC													1488
3270	Thr	Cys		Cys	Met	Pro	Gly		Lys	Gly	Val	His	_	Glu	Leu	Glu	
3271 3272			480					485					490				
3272	ATA	AAT	GAA	TGT	CAG	AGC	AAC	CCT	TGT	GTG	AAC	AAT	GGG	CAG	TGT	GTG	1536
3274	Ile	Asn	Glu	Cys	Gln	Ser	Asn	Pro	Cys	Val	Asn	Asn	Gly	Gln	Cys	Val	
3275		495					500					505					
3276 3277	CATE	א א א א	CTTC	AAT	COTT	mm/a	C A C	TOO	ama	m/cm	CCI	aam	COM	mma	7 CI	aaa	1504
3277				Asn													1584
3279	510	-10			9	515	0111	0,0	204	Cyb	520	110	017	- 110		525	
3280																	
3281				CAG													1632
3282 3283	Pro	Val	Cys	Gln		Asp	Ile	Asp	Asp	_	Ser	Ser	Thr	Pro	_	Leu	
3284					530					535					540		
3285	AAT	GGG	GCA	AAG	TGT	ATC	GAT	CAC	CCG	AAT	GGC	TAT	GAA	TGC	CAG	TGT	1680
3286	Asn	Gly	Ala	Lys	Cys	Ile	Asp	His	Pro	Asn	Gly	Tyr	Glu	Cys	Gln	Cys	
3287				545					550					555			
3288	aaa	3.03	aam	mma	3 CM	aam	ama	mma	mam	~~~	a. a	7 7 C	3 mm	~~~	3 3 C	mam	7.500
3289 3290				TTC Phe													1728
3290	AIa	1111	560	FIIE	1111	СТУ	vai	565	Cys	GIU	GIU	ASII	570	Asp	ASII	СуБ	
3292																	
3293	GAC	CCC	GAT	CCT	TGC	CAC	CAT	GGT	CAG	TGT	CAG	GAT	GGT	ATT	GAT	TCC	1776
3294	Asp		Asp	Pro	Cys	His		Gly	Gln	Cys	Gln	_	Gly	Ile	Asp	Ser	
3295 3296		575					580					585					
3296	TAC	ACC	TGC	ATC	TGC	ААТ	CCC	GGG	TAC	ATG	GGC	GCC	ATC	TGC	AGT	GAC	1824
3298				Ile													2021
3299	590		_		_	595		Ā	_		600			-		605	
3300	~-~		~- -	~			- ~ ~						~	~			
3301 3302				GAA													1872
3302	GIII	TIE	ASP	Glu	610	ıyı	ser	ser	PIO	615	пеп	ASII	Asp	GIĀ	620	Cys	
3304					0_0					0_0					020		
3305				GTC													1920
3306	Ile	Asp	Leu	Val	Asn	Gly	Tyr	Gln		Asn	Cys	Gln	Pro	_	Thr	Ser	
3307				625					630					635			
3308 3309	GGG	СТТ	ТАА	TGT	GAA	ידידע	ΔΑΤ	ידידידי	САТ	GAC	тСт	GCA	ΔСΤ	ממכ	ССТ	тст	1968
3310				Cys													1300
3311	4		640	4				645	- 1	- 4-	4		650			•	
3312																	_
3313				ATC													2016
3314 3315	тте	H1S	GTA	Ile	cys	Met	Asp 660	GTA	тте	Asn	arg	Tyr 665	ser	cys	va⊥	cys	
2213		درن					000					000					

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3316		~~~	~~~			~~~	~-~										_	
3317			GGA														2	2064
3318		Pro	Gly	Phe	Thr		GIn	Arg	Cys	Asn		Asp	Ile	Asp	GLu	-		
3319	670					675					680					685		
3320																		
3321			AAT														2	2112
3322	Ala	Ser	Asn	Pro	_	Arg	Lys	Gly	Ala	Thr	Cys	Ile	Asn	Gly	Val	Asn		
3323					690					695					700			
3324																		
3325			CGC														2	2160
3326	Gly	Phe	Arg	Cys	Ile	Cys	Pro	Glu	Gly	Pro	His	His	Pro	Ser	Cys	Tyr		
3327				705					710					715				
3328																		
3329			GTG														2	2208
3330	Ser	Gln	Val	Asn	Glu	Cys	Leu	Ser	Asn	Pro	Cys	Ile	His	Gly	Asn	Cys		
3331			720					725					730					
3332																		
3333	ACT	GGA	GGT	CTC	AGT	GGA	TAT	AAG	TGT	CTC	TGT	GAT	GCA	GGC	TGG	GTT	2	256
3334	Thr	Gly	Gly	Leu	Ser	Gly	Tyr	Lys	Cys	Leu	Cys	Asp	Ala	Gly	Trp	Val		
3335		735					740					745						
3336																		
3337	GGC	ATC	AAC	TGT	GAA	GTG	GAC	AAA	AAT	GAA	TGC	CTT	TCG	AAT	CCA	TGC	2	304
3338	Gly	Ile	Asn	Cys	Glu	Val	Asp	Lys	Asn	Glu	Cys	Leu	Ser	Asn	Pro	Cys		
3339	750					755					760					765		
3340																		
3341	CAG	AAT	GGA	GGA	ACT	TGT	GAC	AAT	CTG	GTG	AAT	GGA	TAC	AGG	TGT	ACT	2	352
3342	Gln	Asn	Gly	Gly	Thr	Cys	Asp	Asn	Leu	Val	Asn	Gly	Tyr	Arg	Cys	Thr		
3343					770					775					780			
3344																		
3345	TGC	AAG	AAG	GGC	TTT	AAA	GGC	TAT	AAC	TGC	CAG	GTG	AAT	ATT	GAT	GAA	2	400
3346	Cys	Lys	Lys	Gly	Phe	Lys	Gly	Tyr	Asn	Cys	Gln	Val	Asn	Ile	Asp	Glu		
3347				785					790					795				
3348																		
3349	TGT	GCC	TCA	AAT	CCA	TGC	CTG	AAC	CAA	GGA	ACC	TGC	TTT	GAT	GAC	ATA	2	448
3350	Cys	Ala	Ser	Asn	Pro	Cys	Leu	Asn	Gln	Gly	Thr	Cys	Phe	Asp	Asp	Ile		
3351			800					805					810					
3352																		
3353	AGT	GGC	TAC	ACT	TGC	CAC	TGT	GTG	CTG	CCA	TAC	ACA	GGC	AAG	AAT	TGT	2	496
3354	Ser	Gly	Tyr	Thr	Cys	His	Cys	Val	Leu	Pro	Tyr	Thr	Gly	Lys	Asn	Cys		
3355		815					820					825						
3356																		
3357	CAG	ACA	GTA	TTG	GCT	CCC	TGT	TCC	CCA	AAC	CCT	TGT	GAG	AAT	GCT	GCT	2	2544
3358	Gln	Thr	Val	Leu	Ala	Pro	Cys	Ser	Pro	Asn	Pro	Cys	Glu	Asn	Ala	Ala		
3359	830					835					840					845		
3360																		
3361			AAA														2	592
3362	Val	Cys	Lys	Glu	Ser	Pro	Asn	Phe	Glu	Ser	Tyr	Thr	Cys	Leu	Cys	Ala		
3363					850					855					860			
3364																		
3365	CCT	GGC	TGG	CAA	GGT	CAG	CGG	TGT	ACC	ATT	GAC	ATT	GAC	GAG	TGT	ATC	2	640
3366	Pro	Gly	\mathtt{Trp}	Gln	Gly	Gln	Arg	Cys	Thr	Ile	Asp	Ile	Asp	Glu	Cys	Ile		

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3367				865					870					875			
3368 3369	TCC	AAG	CCC	TGC	ATG	AAC	САТ	ССТ	СТС	тсс	СЪТ	אאכ	ACC	CAG	GGC	AGC	2688
3370		Lys															2000
3371		- 4	880	- 4				885		- 2 -			890		1		
3372																	
3373	TAC	ATG	TGT	GAA	TGT	CCA	CCA	GGC	TTC	AGT	GGT	ATG	GAC	TGT	GAG	GAG	2736
3374	Tyr	Met	Cys	Glu	Cys	Pro		Gly	Phe	Ser	Gly		Asp	Cys	Glu	Glu	
3375		895					900					905					
3376	C A C	7 mm	C A III	C T C	шаа	Cmm	aaa	70 70 III	ССШ	шаа	an a	70 70 FTT	007	ООШ	шаа	m.c.m	2704
3377 3378		ATT Ile					_										2784
3379	910	116	ASP	ASP	Cys	915	AIG	A211	FIU	Cys	920	ASII	Gry	GIY	SCI	925	
3380	710					713					720					723	
3381	ATG	GAT	GGA	GTG	AAT	ACT	TTC	TCC	TGC	CTC	TGC	СТТ	CCG	GGT	TTC	ACT	2832
3382		Asp															
3383		•	•		930				•	935	•			-	940		
3384																	
3385	GGG	GAT	AAG	TGC	CAG	ACA	GAC	ATG	AAT	GAG	TGT	CTG	AGT	GAA	CCC	TGT	2880
3386	Gly	Asp	Lys	Cys	Gln	Thr	Asp	Met	Asn	Glu	Cys	Leu	Ser	Glu	Pro	Cys	
3387				945					950					955			
3388																	
3389		AAT															2928
3390	Lys	Asn	_	GLY	Inr	Cys	Ser	_	Tyr	Val	Asn	Ser	_	Thr	Cys	Lys	
3391			960					965					970				
3392 3393	ጥርር	CAG	CCA	CCA	ттт	СЪТ	CCA	CTC	СУТ	тст	GAG	አአሮ	አአሮ	ΔТС	יי א א	GAG	2976
3394		Gln															2370
3395	Cyb	975		0-7		пор	980		*****	Cyb	014	985	1.011		11011	O_u	
3396												,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,					
3397	TGC	ACT	GAG	AGC	TCC	TGT	TTC	AAT	GGT	GGC	ACA	TGT	GTT	GAT	GGG	ATT	3024
3398	Cys	Thr	Glu	Ser	Ser	Cys	Phe	Asn	Gly	Gly	Thr	Cys	Val	Asp	Gly	Ile	
3399	990					995					1000	0				1005	
3400																	
3401		TCC															3072
3402	Asn	Ser	Phe	Ser	_		Cys	Pro	Val	_		Thr	Gly	Ser		_	
3403					1010)				101	5				1020	,	
3404 3405	СТС	CAT	CAC	አጥሮ	א א ידי	CAA	TCC	אככ	тст	СУД	CCA	тсс	СТС	ייי א א	GVG	CCA	3120
3405		His															3120
3407	пси	1125	OIU	1025		OIU	Cys	JCI	1030		110	Cys	пси	1035		Gry	
3408				1020										1000			
3409	ACG	TGT	GTT	GAT	GGC	CTG	GGT	ACC	TAC	CGC	TGC	AGC	TGC	CCC	CTG	GGC	3168
3410		Cys															
3411		=	1040	_	-		_	1045	_	-	=		105			-	
3412																	
3413		ACT															3216
3414	Tyr	Thr	-	Lys	Asn	Cys			Leu	Val	Asn		-	Ser	Arg	Ser	
3415		105	•				1060	י				1069	•				
3416 3417	ממא	TGT	7\7\7\	א א מי	אר אר אר אר אר אר	CCT	л Ст	тст	CITITE	מאמ	71,71,71	7.7.7.	ככיז	C) C	שרכ כ	CAG	3264
2-#T/	CCA	191	www	MMC	WW	331	ACI	191	GII	CAG	WW	WW	GCH	CAG	100	CAG	2204

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3418 3419	Pro Cys 1070	Lys	Asn	Lys	Gly 1075		Cys	Val	Gln	Lys 1080	-	Ala	Glu	Ser	Gln 1085	
3420 3421 3422 3423 3424	TGC CTA Cys Leu				Gly					Tyr					Asn	3312
3425 3426 3427 3428	GTC TCT Val Ser			Ile					Arg					Glu		3360
3429 3430 3431 3432	TTG TGC Leu Cys		His					Ile					Thr			3408
3433 3434 3435 3436	TGT CAG Cys Gln 113	Cys					Thr					Glu				3456
3437 3438 3439 3440	GAT GAG Asp Glu 1150					Pro					Ala					3504
3441 3442 3443	TTC ATT				Arg					Pro					Val	3552
3444 3445 3446 3447	AAC TGT Asn Cys			Glu					Gln					Gln		3600
3448 3449 3450 3451	GGA GGC Gly Gly		Cys					Asn					Ser			3648
3452 3453 3454 3455	CCA GGC Pro Gly 121	Thr					Cys					Asp				3696
3456 3457 3458 3459	CGG GGT Arg Gly 1230					Asn					Met					3744
3460 3461 3462 3463 3464	GGC TAC				Cys					Ala					Glu	3792
3464 3465 3466 3467 3468	GGA GAC Gly Asp			Glu					Pro					Gly		3840

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3469					CAG												3888
3470	Leu	Asp	Cys	Ile	Gln	Leu	Thr	Asn	Asp	Tyr	Leu	Cys	Val	Cys	Arg	Ser	
3471			1280)				1285	5				1290)			
3472																	
3473					CGG												3936
3474	Ala			GLY	Arg	Hıs	-		Thr	Phe	Val	_		Cys	Pro	Gln	
3475		129	>				1300)				1305	•				
3476	» ma	aaa	maa	ama	7 7 M	GG 7	aaa	3 CI CI	mam	aam	ama	aaa	3 CI	220	3 mg	aam	2004
3477 3478					AAT												3984
3479	1310		Cys	цец	Asn	1315		1111	Cys	AIA	1320		ser	ASII	Met	1325	
3480	131(,				131:	,				1320	,				1325	
3481	САТ	сст	ጥጥር	עיייע	TGC	ССТ	ጥርሞ	כככ	CCG	CCA	արար	ייירר	ccc	CCA	ACC	TCC	4032
3482					Cys												4032
3483	пор	0 - y	1		1330	_	Cys	110	110	1335		DCI	O _T y	AIG	134	_	
3484											•					•	
3485	CAG	AGC	AGC	TGT	GGA	CAA	GTG	AAA	TGT	AGG	AAG	GGG	GAG	CAG	TGT	GTG	4080
3486					Gly												
3487				1345				•	1350	_	-	•		1355	_		
3488																	
3489	CAC	ACC	GCC	TCT	GGA	CCC	CGC	TGC	TTC	TGC	CCC	AGT	CCC	CGG	GAC	TGC	4128
3490	His	Thr	Ala	Ser	Gly	Pro	Arg	Cys	Phe	Cys	Pro	Ser	Pro	Arg	Asp	Cys	
3491			1360)				1365	5				1370)			
3492																	
3493					GCC												4176
3494	Glu		_	Cys	Ala	Ser	Ser	Pro	Cys	Gln	His	Gly	Gly	Ser	Cys	His	
3495		137	5				1380)				1385	5				
3496																	
3497					CCT												4224
3498			Arg	GIn	Pro		_	Tyr	Ser	Cys		-	Ата	Pro	Pro		
3499 3500	1390	,				1395	•				1400)				1405	
3500	TCC	~~-															
3501	100		אככ	CCC	m/cm	C 7 7	CTC	TIAC	700	CCA	aaa	ccc	אככ	אממ	COTT	COTT	4272
	Sar				TGT												4272
	Ser				Cys	Glu				Ala	Pro				Pro	Pro	4272
3503	Ser					Glu					Pro					Pro	4272
3503 3504		Gly	Ser	Arg	Cys 1410	Glu O	Leu	Tyr	Thr	Ala 1415	Pro	Pro	Ser	Thr	Pro 1420	Pro)	
3503 3504 3505	GCC	Gly ACC	Ser TGT	Arg CTG	Cys 1410 AGC	Glu) CAG	Leu TAT	Tyr TGT	Thr	Ala 1415 GAC	Pro AAA	Pro GCT	Ser CGG	Thr GAT	Pro 1420 GGC	Pro) GTC	4272 4320
3503 3504	GCC	Gly ACC	Ser TGT	Arg CTG	Cys 1410 AGC Ser	Glu) CAG	Leu TAT	Tyr TGT	Thr	Ala 1415 GAC Asp	Pro AAA	Pro GCT	Ser CGG	Thr GAT	Pro 1420 GGC Gly	Pro) GTC	
3503 3504 3505 3506	GCC	Gly ACC	Ser TGT	Arg CTG Leu	Cys 1410 AGC Ser	Glu) CAG	Leu TAT	Tyr TGT	Thr GCC Ala	Ala 1415 GAC Asp	Pro AAA	Pro GCT	Ser CGG	Thr GAT Asp	Pro 1420 GGC Gly	Pro) GTC	
3503 3504 3505 3506 3507	GCC Ala	Gly ACC Thr	Ser TGT Cys	Arg CTG Leu 1425	Cys 1410 AGC Ser	Glu) CAG Gln	Leu TAT Tyr	Tyr TGT Cys	Thr GCC Ala 1430	Ala 1415 GAC Asp	Pro AAA Lys	Pro GCT Ala	Ser CGG Arg	Thr GAT Asp 1435	Pro 1420 GGC Gly	Pro) GTC Val	
3503 3504 3505 3506 3507 3508	GCC Ala TGT	Gly ACC Thr	Ser TGT Cys	Arg CTG Leu 1425	Cys 1410 AGC Ser	Glu CAG Gln	Leu TAT Tyr	Tyr TGT Cys CAT	Thr GCC Ala 1430 GCC	Ala 1415 GAC Asp)	Pro AAA Lys CAG	Pro GCT Ala TGG	Ser CGG Arg	Thr GAT Asp 1435	Pro 1420 GGC Gly GGT	Pro) GTC Val GAC	4320
3503 3504 3505 3506 3507 3508 3509	GCC Ala TGT	Gly ACC Thr	Ser TGT Cys	CTG Leu 1425 GCC Ala	Cys 1410 AGC Ser 5	Glu CAG Gln	Leu TAT Tyr	Tyr TGT Cys CAT	Thr GCC Ala 1430 GCC Ala	Ala 1415 GAC Asp)	Pro AAA Lys CAG	Pro GCT Ala TGG	Ser CGG Arg	GAT Asp 1435 GGG Gly	Pro 1420 GGC Gly GGT	Pro) GTC Val GAC	4320
3503 3504 3505 3506 3507 3508 3509 3510 3511 3512	GCC Ala TGT Cys	Gly ACC Thr GAT Asp	TGT Cys GAG Glu 1440	CTG Leu 1425 GCC Ala	Cys 1410 AGC Ser TGC	CAG Gln AAC Asn	TAT Tyr AGC Ser	Tyr TGT Cys CAT His 1445	GCC Ala 1430 GCC Ala	Ala 1415 GAC Asp O TGC Cys	Pro AAA Lys CAG Gln	Pro GCT Ala TGG Trp	CGG Arg GAT Asp 1450	GAT Asp 1435 GGG Gly	Pro 1420 GGC Gly GGT GGY	Pro) GTC Val GAC Asp	4320
3503 3504 3505 3506 3507 3508 3509 3510 3511 3512 3513	GCC Ala TGT Cys	ACC Thr GAT Asp	TGT Cys GAG Glu 1440	CTG Leu 1425 GCC Ala	Cys 1410 AGC Ser TGC Cys	CAG Gln AAC Asn	TAT Tyr AGC Ser	TGT Cys CAT His 1445	GCC Ala GCC Ala TGG	Ala 1415 GAC Asp TGC Cys	AAA Lys CAG Gln	Pro GCT Ala TGG Trp	CGG Arg GAT Asp 1450	GAT Asp 1435 GGG Gly TCC	GGC Gly GGT Gly CCA	Pro O GTC Val GAC Asp	4320
3503 3504 3505 3506 3507 3508 3509 3510 3511 3512 3513 3514	GCC Ala TGT Cys	ACC Thr GAT Asp	TGT Cys GAG Glu 1440 CTC Leu	CTG Leu 1425 GCC Ala	Cys 1410 AGC Ser TGC	CAG Gln AAC Asn	TAT Tyr AGC Ser AAC Asn	TGT Cys CAT His 1445 CCC Pro	GCC Ala GCC Ala TGG	Ala 1415 GAC Asp TGC Cys	AAA Lys CAG Gln	Pro GCT Ala TGG Trp TGC Cys	CGG Arg GAT Asp 1450 TCC Ser	GAT Asp 1435 GGG Gly TCC	GGC Gly GGT Gly CCA	Pro O GTC Val GAC Asp	4320 4368
3503 3504 3505 3506 3507 3508 3509 3510 3511 3512 3513 3514 3515	GCC Ala TGT Cys	ACC Thr GAT Asp	TGT Cys GAG Glu 1440 CTC Leu	CTG Leu 1425 GCC Ala	Cys 1410 AGC Ser TGC Cys	CAG Gln AAC Asn	TAT Tyr AGC Ser	TGT Cys CAT His 1445 CCC Pro	GCC Ala GCC Ala TGG	Ala 1415 GAC Asp TGC Cys	AAA Lys CAG Gln	Pro GCT Ala TGG Trp	CGG Arg GAT Asp 1450 TCC Ser	GAT Asp 1435 GGG Gly TCC	GGC Gly GGT Gly CCA	Pro O GTC Val GAC Asp	4320 4368
3503 3504 3505 3506 3507 3508 3509 3510 3511 3512 3513 3514 3515 3516	GCC Ala TGT Cys TGT Cys	Gly ACC Thr GAT Asp TCT Ser 1459	TGT Cys GAG Glu 1440 CTC Leu	CTG Leu 1425 GCC Ala) ACC Thr	Cys 1410 AGC Ser TGC Cys ATG Met	CAG Gln AAC Asn GAG Glu	TAT Tyr AGC Ser AAC Asn 1460	TGT Cys CAT His 1445 CCC Pro	GCC Ala 1430 GCC Ala TGG	GAC Asp TGC Cys	AAA Lys CAG Gln AAC	GCT Ala TGG Trp TGC Cys 1465	CGG Arg GAT Asp 1450 TCC Ser	GAT Asp 1435 GGG Gly TCC Ser	GGC Gly GGT Gly CCA Pro	GTC Val GAC Asp CTT Leu	4320 4368 4416
3503 3504 3505 3506 3507 3508 3509 3510 3511 3512 3513 3514 3515 3516 3517	GCC Ala TGT Cys TGT Cys	Gly ACC Thr GAT Asp TCT Ser 1459	TGT Cys GAG Glu 1440 CTC Leu	CTG Leu 1425 GCC Ala) ACC Thr	Cys 1410 AGC Ser TGC Cys ATG Met	CAG Gln AAC Asn GAG Glu	TAT Tyr AGC Ser AAC Asn 1460	TGT Cys CAT His 1445 CCC Pro	GCC Ala 1430 Ala TGG Trp	GAC Asp TGC Cys	AAA Lys CAG Gln AAC Asn	GCT Ala TGG Trp TGC Cys 1465	CGG Arg GAT Asp 1450 TCC Ser	GAT Asp 1435 GGG Gly TCC Ser	GGC Gly GGT Gly CCA Pro	Pro O GTC Val GAC Asp CTT Leu ACG	4320 4368
3503 3504 3505 3506 3507 3508 3509 3510 3511 3512 3513 3514 3515 3516	GCC Ala TGT Cys TGT Cys	Gly ACC Thr GAT Asp TCT Ser 1459 TGC Cys	TGT Cys GAG Glu 1440 CTC Leu	CTG Leu 1425 GCC Ala) ACC Thr	Cys 1410 AGC Ser TGC Cys ATG Met	CAG Gln AAC Asn GAG Glu	TAT Tyr AGC Ser AAC Asn 1460	TGT Cys CAT His 1445 CCC Pro	GCC Ala 1430 Ala TGG Trp	GAC Asp TGC Cys	AAA Lys CAG Gln AAC Asn	GCT Ala TGG Trp TGC Cys 1465	CGG Arg GAT Asp 1450 TCC Ser	GAT Asp 1435 GGG Gly TCC Ser	GGC Gly GGT Gly CCA Pro	Pro O GTC Val GAC Asp CTT Leu ACG	4320 4368 4416

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3520																	
3521														AGC			4512
3522	Val	Glu	Cys	Leu			Asn	Phe	Glu			Gly	Asn	Ser	_		
3523					1490)				1495	5				1500)	
3524																	
3525														AAC			4560
3526	Cys	Lys	Tyr		_	Tyr	Cys	Ala			Phe	Lys	Asp	Asn		Cys	
3527				150	5				1510)				1519	5		
3528	~																
3529														CTG			4608
3530	Asn	GIn			Asn	Ser	GIu			GLY	Trp	Asp		Leu	Asp	Cys	
3531			1520)				1525)				1530	0			
3532	~~~	~~~	~~~	~	~~~	~~~		~~~	~~-	~	~~~		~~~	~~~			
3533														GTT			4656
3534	Ala		_	GIn	Pro	GIu			Ala	GIu	Gly			Val	Ile	Val	
3535		1535)				1540)				1545	•				
3536	am.	mma	3 ma	~~~	00m	~~~	~~~	ОПО	ama	G 2 G	a	aam	~~~				4504
3537														AGC			4704
3538			мес	Pro	PIO			Leu	ьeu	GIII			arg	Ser	Pne		
3539 3540	1550	J				1555	•				1560	U				1565	
	aaa	~~~	ama	aam	7.00	аша	аша	a	700	770	аша	aaa	7 mm	770	aaa	GR G	4750
3541 3542														AAG			4752
	Arg	Ата	ьeu	GIY			ьeu	nis	TIIL			Arg	TTE	Lys	_	_	
3543 3544					1570	,				1575)				1580	,	
3544	TOO	CAC	aaa	C1 N N	CTC	א יייר	CTC	π ν.α	COO	T N T	תו א תו	COT	ana.	AAG	תרים	COT	4800
3545														Lys			4000
3547	261	GIII	СТУ	158		Mec	vai	TYL	1590	_	TYL	GIY	GIU	1595		Ala	
3548				150.	,				1330	J				139.	,		
3549	GCT	ΔТС	ΔΔG	מממ	CAG	AGG	ΔТС	מרמ	רפר	AGA	TCC	Стт	ССТ	GGT	CDD	CAA	4848
3550														Gly			1010
3551	AIU	1100	1600	_	0111	nr 9	1100	1609	-	A-9	JCI	пси	1610	_	OIU	GIII	
3552				•										•			
3553	GAA	CAG	GAG	GTG	GCT	GGC	тст	ΔΔΔ	GTC	ттт	СТС	GAA	בתת	GAC	AAC	CGC	4896
3554														Asp			
3555		1615				0-1	1620	_				162				5	
3556			-					_					-				
3557	CAG	TGT	GTT	CAA	GAC	TCA	GAC	CAC	TGC	TTC	AAG	AAC	ACG	GAT	GCA	GCA	4944
3558														Asp			_
3559	1630	_			-	1635	_		•		1640			-		1645	
3560																	
3561	GCA	GCT	CTC	CTG	GCC	TCT	CAC	GCC	ATA	CAG	GGG	ACC	CTG	TCA	TAC	CCT	4992
3562	Ala	Ala	Leu	Leu	Ala	Ser	His	Ala	Ile	Gln	Gly	Thr	Leu	Ser	Tyr	Pro	
3563					1650					1655	_				1660		
3564																	
3565	CTT	GTG	TCT	GTC	GTC	AGT	GAA	TCC	CTG	ACT	CCA	GAA	CGC	ACT	CAG	CTC	5040
3566	Leu	Val	Ser	Val	Val	Ser	Glu	Ser	Leu	Thr	Pro	Glu	Arg	Thr	Gln	Leu	
3567				166	5				1670	0				1675	5		
3568																	
3569														ATT			5088
3570	Leu	Tyr	Leu	Leu	Ala	Val	Ala	Val	Val	Ile	Ile	Leu	Phe	Ile	Ile	Leu	

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3571 3572			1680)				1685	5				169	0			
3572	СТС	GGG	СΤΔ	ΔТС	ATG	GCA	ΔΔΔ	CGA	ΔΔG	ССТ	ΔΔG	СУТ	GGC	тст	СТС	TGG	5136
3574					Met												3130
3575		1695					1700	_	-1-	9	-,-	170	_	J U _		P	
3576		103					_,,,,										
3577	СТС	ССТ	GAA	GGT	TTC	ΔСТ	СТТ	CGC	CGA	САТ	GCA	AGC	Тαα	CAC	ΔAG	ССТ	5184
3578					Phe												3101
3579	1710			01	- 110	171		9	••• 9		1720			*****	_,,,	1725	
3580						_,_,										1,23	
3581	ССТ	GAG	$CC\Delta$	GTG	GGA	CAG	САТ	сст	стс	GGG	СТС	מממ	דע ע	СТС	тса	GTG	5232
3582					Gly												3232
3583	- 9			V C4.11	1730		пор	n_u	٧٠٠	1735		טעם	ADII	Lou	1740		
3584					1,5	•				1,50							
3585	CAA	GTC	тса	GAA	GCT	AAC	СТД	ΔТТ	GGT	ΔСТ	GGA	ACA	AGT	GAA	CAC	TGG	5280
3586					Ala												3200
3587	0	, u _	501	174!		11011		110	1750		017	****	501	175!		119	
3588									1,5	•				_,_,	-		
3589	GTC	GAT	GAT	GAA	GGG	CCC	CAG	CCA	AAG	AAA	GTA	AAG	GCT	GAA	GAT	GAG	5328
3590					Gly												
3591		<u>r</u>	1760		1			176	-	-1-		_1	1770				
3592									-								
3593	GCC	TTA	CTC	TCA	GAA	GAA	GAT	GAC	CCC	ATT	GAT	CGA	CGG	CCA	TGG	ACA	5376
3594					Glu												
3595		1775					1780	_			•	178	_		_		
3596																	
3597	CAG	CAG	CAC	CTT	GAA	GCT	GCA	GAC	ATC	CGT	AGG	ACA	CCA	TCG	CTG	GCT	5424
3598	Gln	Gln	His	Leu	Glu	Ala	Ala	Asp	Ile	Arq	Arq	Thr	Pro	Ser	Leu	Ala	
3599	1790					179		•			1800					1805	
3600																	
3601	CTC	ACC	CCT	CCT	CAG	GCA	GAG	CAG	GAG	GTG	GAT	GTG	TTA	GAT	GTG	AAT	5472
3602	Leu	Thr	Pro	Pro	Gln	Ala	Glu	Gln	Glu	Val	Asp	Val	Leu	Asp	Val	Asn	
3603					1810)				1815	5				1820)	
3604																	
3605	GTC	CGT	GGC	CCA	GAT	GGC	TGC	ACC	CCA	TTG	ATG	TTG	GCT	TCT	CTC	CGA	5520
3606	Val	Arg	Gly	Pro	Asp	Gly	Cys	Thr	Pro	Leu	Met	Leu	Ala	Ser	Leu	Arg	
3607				182	5				1830)				183	5		
3608																	
3609					GAT												5568
3610	Gly	Gly	Ser	Ser	Asp	Leu	Ser	Asp	Glu	Asp	Glu	Asp	Ala	Glu	Asp	Ser	
3611			1840)				1845	5				1850	0			
3612																	
3613					ATC												5616
3614	Ser			Ile	Ile	Thr	_		Val	Tyr	Gln	_		Ser	Leu	Gln	
3615		185	•				1860	ט				186	>				
3616	~~~	~~	3.00	a	~~~		~~=	~-~	3 P ~	~~~	~~	~-~	~~~	~~-	~~~	000	
3617					CGG	_			_				_				5664
3618			Inr	Asp	Arg		_	GLU	мес	Α⊥а			ьeu	ΑΙα	Α⊥а	_	
3619 3620	1870	J				187	•				1880	J				1885	
3620	ጥ አ ር ር	ጥርን	ccc	CCT	GAT	ССТ	מממ	አአሮ	CCT	CITIC	CITIC	CAT	מכיז	CCT	ממא	CAT	5712
J U Z I	IAC	I CM	CGG	301	GMI	901	300	AAG	CGI		CIG	GMI	CCA	931	CH	OAI	J/12

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3622 3623 3624	Tyr Se	er Arg	Ala	Asp 1890		Ala	Lys	Arg	Leu 1899		Asp	Ala	Gly	Ala 1900	_	
3625 3626 3627 3628	GCC A			Asp					Cys					Ala		5760
3629 3630 3631 3632	GCA GG Ala A		Ala					Gln					Asn			5808
3633 3634 3635 3636		AT CTA sp Leu 935					Asn					Pro				5856
3637 3638 3639 3640	GCT GG Ala Al 1950					Glu					Glu					5904
3641 3642 3643 3644	CAA GO				Ala					${\tt Gly}$					His	5952
3645 3646 3647 3648	TGG GG			Val					Ala					Leu		6000
3649 3650 3651 3652	AAT GO Asn G		Asn					Asp					Thr			6048
3653 3654 3655 3656		TT GCT eu Ala 015					Ser					Lys				6096
3657 3658 3659 3660	GAC CA Asp H: 2030					Asp					Met					6144
3661 3662 3663 3664		AT GTG sp Val			Asp					Asp					Leu	6192
3665 3666 3667 3668	GAT GAT GAT	AA TAC lu Tyr		Val					Pro					Thr		6240
3669 3670 3671 3672	GCT CT Ala Le		Pro					Pro					Leu			6288

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3673 3674 3675 3676			Lys Ser		CCC AGT GCC Pro Ser Ala 2105		6336
3677 3678 3679 3680					GAG GCA AAG Glu Ala Ly: O		6384
3681 3682 3683 3684		Lys Lys			AAG GTC CAL Lys Val Gli		6432
3685 3686 3687 3688				Asp Ser	CTA GAA TC' Leu Glu Se: 21:	r Pro His	6480
3689 3690 3691 3692	Thr Tyr V				ATT ACA TCC Ile Thr Sec 2170		6528
3693 3694 3695 3696			Pro Met		ACT GCC GCC Thr Ala Ala 2185		6576
3697 3698 3699 3700					TCT AAC CT Ser Asn Le		6624
3701 3702 3703 3704		His Gly			CTT CCC TC		6672
3705 3706 3707 3708				Ser Pro	GGC AGT GGG Gly Ser Gly 22	y Ser Ala	6720
3709 3710 3711 3712	Gly Ser I				CCA GCA GA' Pro Ala As ₁ 2250		6768
3713 3714 3715 3716			Thr Gln		GAG ATG TT Glu Met Pho 2265		6816
3717 3718 3719 3720					ATA GCT CC0 Ile Ala Pro O		6864
3721 3722 3723		Lys His			CGG GAG CCC Arg Glu Pro		6912

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3724							
3725	CCC ATT G	TG ACT TTC C	AG CTC ATC	CCT AAA	GGC AGT ATT	GCC CAA CCA	6960
3726		al Thr Phe G					
3727		2305		2310	_	2315	
3728							
3729	GCG GGG GG	CT CCC CAG C	CT CAG TCC	ACC TGC	CCT CCA GCT	GTT GCG GGC	7008
3730	Ala Gly Al	la Pro Gln P	ro Gln Ser	Thr Cys	Pro Pro Ala	Val Ala Gly	
3731	23	320	232	5	2330)	
3732							
3733	CCC CTG CC	CC ACC ATG T	AC CAG ATT	CCA GAA	ATG GCC CGT	TTG CCC AGT	7056
3734	Pro Leu Pr	ro Thr Met T	yr Gln Ile	Pro Glu	Met Ala Arg	Leu Pro Ser	
3735	2335		2340		2345		
3736							
3737		TC CCC ACT G					7104
3738	Val Ala Ph	he Pro Thr A	la Met Met	Pro Gln	Gln Asp Gly	Gln Val Ala	
3739	2350	2	355		2360	2365	
3740							
3741		TT CTC CCA G					7152
3742	Gin Thr I	le Leu Pro A	la Tyr His				
3743		2370		2375		2380	
3744			~- ~- ~ ~-		~~~ ~~~		
3745		CA CCC CCT T					7200
3746	Tyr Pro Tr	hr Pro Pro S	er Gin His	_	Ala Ser Ser		
3747		2385		2390		2395	
3748	C2C CC2 20	an acc nam a	7.C 7.Cm CCm	ana ama	ana aam ana	CAM CCC MAC	7040
3749 3750		CA CCC AGT C					7248
3751		hr Pro Ser H 400	240!		2410 2410	-	
3751	24	400	240:	.	2410	,	
3753	כדב אכא כנ	CA TCC CCA G	ልር ጥርጥ ሮርጥ	GAC CAG	שמב שכא אפש	יירא יירא כככ	7296
3754		ro Ser Pro G					7230
3755	2415	TO BEL FIO G	2420	ASP GIII	2425	Der Der Fro	
3756	2113		2420		2123		
3757	CAC TCT GO	CT TCT GAC T	GG TCA GAT	GTG ACC	ACC AGC CCT	ACC CCT GGG	7344
3758		la Ser Asp T					
3759	2430	-	435		2440	2445	
3760							
3761	GGT GCT GC	GA GGA GGT C	AG CGG GGA	CCT GGG	ACA CAC ATG	TCT GAG CCA	7392
3762	Gly Ala G	ly Gly Gly G	ln Arg Gly	Pro Gly	Thr His Met	Ser Glu Pro	
3763	_	2450		2455		2460	
3764							
3765	CCA CAC A	AC AAC ATG C	AG GTT TAT	GCG TGAG	AGAGTC CACCI	CCAGT	7439
3766	Pro His As	sn Asn Met G	ln Val Tyr	Ala			
3767		2465		2470			
3768							
3769	GTAGAGACAT	T AACTGACTTT	TGTAAATGC'	r gctgagg	AAC AAATGAAG	GT CATCCGGGAG	7499
3770							
3771	AGAAATGAAG	G AAATCTCTGG	AGCCAGCTT	C TAGAGGT	AGG AAAGAGAA	AGA TGTTCTTATT	7559
3772 3773 CAGATAATGC AAGAGAAGCA ATTCGTCAGT TTCACTGGGT ATCTGCAAGG CTTATTGATT 7619							
3773	CAGATAATG	C AAGAGAAGCA	ATTCGTCAG'	r TTCACTG	GGT ATCTGCA	AGG CTTATTGATT	7619
3774							

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3775	ATTCTAATCT	AATAAGACAA	GTTTGTGGAA	ATGCAAGATG	AATACAAGCC	TTGGGTCCAT	7679
3776 3777	GTTTACTCTC	TTCTATTTGG	AGAATAAGAT	GGATGCTTAT	TGAAGCCCAG	ACATTCTTGC	7739
3778							
3779 3780	AGCTTGGACT	GCATTTTAAG	CCCTGCAGGC	TTCTGCCATA	TCCATGAGAA	GATTCTACAC	7799
3781	TAGCGTCCTG	TTGGGAATTA	TGCCCTGGAA	TTCTGCCTGA	ATTGACCTAC	GCATCTCCTC	7859
3782	CITIC CITITIC C T C	3 mm/cmmmm/cm		ma ammmaam	mmma a a a a a a	macama a mma	7010
3783	CTCCTTGGAC	ATTCTTTTGT	CTTCATTTGG	TGCTTTTGGT	TTTGCACCTC	TCCGTGATTG	7919
3784 3785	ma a a a a a a a a a	3 C C 3 M C M M 3 M	7000077070	ammama amm	mma 3 ma 3 mma	maaaaaa maa	7070
	TAGCCCTACC	AGCATGTTAT	AGGGCAAGAC	CTTTGTGCTT	TIGATCATIC	TGGCCCATGA	7979
3786 3787	7 7 C C 7 7 C C C C C C C C C C C C C C	aamamaammm	aaaamaamam	CDD CCCCCD A	maaammaa a	mamar ar raa	0000
3788	AAGCAACIII	GGTCTCCTTT	CCCCTCCTGT	CTTCCCGGTA	TCCCTTGGAG	TCTCACAAGG	8039
3789	ጥጥጥ አ ረጥጥጥረረ	TATGGTTCTC	7007077700	መመመረስ አረመስመ	<u>പന്നവനനന്നന</u>	TGGAAAATGG	8099
3790	IIIACIIIGG	TAIGGITCIC	AGCACAAACC	IIICAAGIAI	GIIGIIICII	IGGAAAAIGG	6033
3791	እ <i>ር</i> እጥ እርጥር ጥ እ	TTGTGTTCTC	<u>רייוברי</u> א יייא יייא ייי	CATTCCTCCA	CACACAACCC	CACAACAATA	8159
3792	ACATACIGIA	TIGIGITETE	CIGCAIAIAI	CATICCIGGA	GAGAGAAGGG	GAGAAGAATA	0133
3792		ACAAATTTTG	CCCCCACCAC	አጥሮርርጥጥር አ አ	СУСССТССУС	ር ጥጥ እ አ ጥጥጥጥጥ	8219
3794	CITITCTICA	ACAAATITIG	GGGGCAGGAG	AICCCIICAA	GAGGCIGCAC	CITAATITI	0219
3795	<u>כייייכייכייכייכ</u>	TGCAGGTCTT	CATATAAAACT	יייי ארכא כבא א	СЛЛСССТСТС	አረ ጥጥጥረጥጥረ ጥ	8279
3796	CIIGICIGIG	IGCAGGICII	CATATAAACT	TIACCAGGAA	GAAGGGIGIG	AGIIIGIIGI	02/3
3797	ጥጥጥርጥረጥረ ጥ	ATGGGCCTGG	тсастатааа	Շ փարար ձարարար ձարարարության անագարարության անագարարարության անագարարության անագարարարության անագարարության անագարար անագարարարարության անագարարար անագարարարարության անագարարար անա	талтлатста	ピープリング ロック・ファック ロック ロック・ファック ロック ロック・ファック ロック ロック ロック ロック ロック ロック ロック ロック ロック ロ	8339
3798	1111010101	AIGGGCCIGG	TCAGTGTAAA	GIIIIAICCI	IGNINGICIA	GIIACIAIGA	0337
3799	СССТССССДС	TTTTTTAAAA	CCDGDDDDG	מייייממא איימ	ттссаатсас	CAAGAGACAA	8399
3800	CCCTCCCCAC	IIIIIIAAAA	ссномимо	GIIIGGAAIG	TIGOARIOAC	CAMONONCAM	0377
3801	стта а стсст	GCAAGAGCCA	GTTACCCACC	СУСУССТССС	ССТАСТТССТ	CCCAACCATT	8459
3802	GITAACICGI	OCAMONOCCA	GITACCCACC	CACAGGICCC	CCIACTICCI	GCCAAGCATT	0437
3803	ССУТТСУСТС	CCTGTATGGA	Δ	СССДСДТСТС	<u>አ</u> ርር አጥጥር ጥ አር	$GCCTGTTTC\Delta$	8519
3804	centronero	CCIGIAIGGA	ACACATITOT	CCCHGHICIG	AGENTICIAG	decidiffen	0317
3805	СТСАСТСАСС	CAGCATATGA	ΔΑСΤΑGΤСΤΤ	ΔΑСΤΩΤΤΩΔΩ	CCդերե CCդերե CCդերե CCդերե CCդերե CCդերե CCդերե CCդերե CCդերե CCդերե CCդերե CCդերե CCդերե CCդերե CCդերե CCդերե CCդե CCդ	САТАТССАСА	8579
3806	01001000	C				CITITITE COLICIT	03/3
3807	GAAGACACTG	TCTCAAATGT	TGTACCCTTG	CCATTTAGGA	CTGAACTTTC	CTTAGCCCAA	8639
3808							
3809	GGGACCCAGT	GACAGTTGTC	TTCCGTTTGT	CAGATGATCA	GTCTCTACTG	ATTATCTTGC	8699
3810							
3811	TGCTTAAAGG	CCTGCTCACC	AATCTTTCTT	TCACACCGTG	TGGTCCGTGT	TACTGGTATA	8759
3812							
3813	CCCAGTATGT	TCTCACTGAA	GACATGGACT	TTATATGTTC	AAGTGCAGGA	ATTGGAAAGT	8819
3814							
3815	TGGACTTGTT	TTCTATGATC	CAAAACAGCC	CTATAAGAAG	GTTGGAAAAG	GAGGAACTAT	8879
3816							
3817	ATAGCAGCCT	TTGCTATTTT	CTGCTACCAT	TTCTTTTCCT	CTGAAGCGGC	CATGACATTC	8939
3818							
3819	CCTTTGGCAA	CTAACGTAGA	AACTCAACAG	AACATTTTCC	TTTCCTAGAG	TCACCTTTTA	8999
3820							
3821	GATGATAATG	GACAACTATA	GACTTGCTCA	TTGTTCAGAC	TGATTGCCCC	TCACCTGAAT	9059
3822							
3823	CCACTCTCTG	TATTCATGCT	CTTGGCAATT	TCTTTGACTT	TCTTTTAAGG	GCAGAAGCAT	9119
3824							
3825	TTTAGTTAAT	TGTAGATAAA	GAATAGTTTT	CTTCCTCTTC	TCCTTGGGCC	AGTTAATAAT	9179

RAW SEQUENCE LISTING PATENT APPLICATION US/08/083,590

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3826							
3827	TGGTCCATGG	CTACACTGCA	ACTTCCGTCC	AGTGCTGTGA	TGCCCATGAC	ACCTGCAAAA	9239
3828							
3829	TAAGTTCTGC	CTGGGCATTT	TGTAGATATT	AACAGGTGAA	TTCCCGACTC	TTTTGGTTTG	9299
3830							
3831	AATGACAGTT	CTCATTCCTT	CTATGGCTGC	AAGTATGCAT	CAGTGCTTCC	CACTTACCTG	9359
3832							
3833	ATTTGTCTGT	CGGTGGCCCC	ATATGGAAAC	CCTGCGTGTC	TGTTGGCATA	ATAGTTTACA	9419
3834							
3835	AATGGTTTTT	TCAGTCCTAT	CCAAATTTAT	TGAACCAACA	AAAATAATTA	CTTCTGCCCT	9479
3836	G3 G3 G3 5 GG3	~	~~~~~				
3837	GAGATAAGCA	GATTAAGTTT	GTTCATTCTC	TGCTTTATTC	TCTCCATGTG	GCAACATTCT	9539
3838	CECT CCCECE		CC2 2 2 C2 FFFF	M. M. C. I. M. C.	33 = 0 0 = 0 3 0 =	CE CE C C C CE	
3839 3840	GTCAGCCTCT	TTCATAGTGT	GCAAACATTT	TATCATTCTA	AATGGTGACT	CTCTGCCCTT	9599
3841	CC A CCC A TITUT	ATTATTCACA	an maaaan an	3 CC 3 M C C	3 maa 3 aaama	3 CC3 TCCTCT	0650
3842	GGACCCATTI	ATTATTCACA	GAIGGGGAGA	ACCIAICIGC	AIGGACCCIC	ACCATCCTCT	9659
3843	GTGCAGCACA	CACAGTGCAG	GGAGCCAGTG	GCGATGGCGA	TGACTTTCTT	CCCCTGGGAA	9719
3844	GIGCAGCACA	CACAGIGCAG	GGAGCCAGIG	GCGAIGGCGA	IGACITICIT	CCCCIGGGAA	3/13
3845	TTCC						9723
3846	1100						7123
3847							

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/08/083,590

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APPLICATION NUMBER FILING DATE PRIOR APPLICATION DATA

SEQUENCE CORRECTION REPORT PATENT APPLICATION US/08/083,590

DATE: 12/16/93 TIME: 13:16:03

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